

**Regulation of Olfactory Stem Cells and Neurogenesis by Primary Cilia and the Hedgehog Pathway**

**by**

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## ABSTRACT

The olfactory epithelium (OE) is one of the few tissues to undergo constitutive neurogenesis throughout the mammalian lifespan. It contains multiple cell types including olfactory sensory neurons (OSNs) that are replaced by two populations of basal stem cells – frequently dividing globose basal cells (GBCs), and quiescent horizontal basal cells (HBCs). Strikingly, the mechanisms that control stem cell activation and proliferation, during normal OE homeostasis and in response to injury remain largely unexplored. My data indicate that HBCs possess primary cilia, cellular organelles that regulate the activity of multiple signaling pathways, including Hedgehog (HH) signaling. The HH pathway is required for the formation, survival, and activity of stem/progenitor cell populations in several adult tissues, making it an attractive candidate for HBC regulation. The goals of this dissertation are: 1) to investigate the role of primary cilia in HBC-driven olfactory neurogenesis and 2) to explore the contribution of HH signaling to HBC function.

My data indicate that HBC-specific deletion of the ciliary gene *Ift88* effectively abrogates primary cilia. Interestingly, the loss of HBC cilia did not affect HBC cell numbers or maintenance of the adult OE, but dramatically impaired the regeneration of OSNs following injury. Furthermore, the loss of cilia during development resulted in region-specific decreases in neurogenesis, implicating HBCs in OE establishment. These results demonstrate a novel role for primary cilia in olfactory neurogenesis and suggest a role for primary cilia in HBC activation, proliferation, and differentiation.

My data also demonstrate that HH pathway components are expressed in the adult OE. Specifically, the HH transcription factors, *Gli2* and *Gli3* are selectively expressed in HBCs, implicating HH signaling in the control of HBC function. Constitutive *Gli2* activation in HBCs resulted in hyperproliferation and loss of neuronal cells, and also impaired OE regeneration following injury. Surprisingly, constitutive *Gli2* repression in HBCs did not alter OE maintenance, but did impair injury-induced OE regeneration. These results suggest a novel role for HH signaling, and specifically *Gli2*, in HBC regulation during OE homeostasis and regeneration. Overall, this work defines novel roles for primary cilia and HH signaling in HBC-mediated regulation of the mammalian OE.

## **CHAPTER I:**

### **Introduction**

#### **1.1 Abstract**

An appreciation of olfaction, or the sense of smell, and its importance across species dates back to ancient civilizations. This appreciation has grown with recent advances in technology and olfactory research. The sense of smell relies on olfactory sensory neurons (OSNs) in the olfactory epithelium (OE) that project compartmentalized organelles, called cilia into the nasal cavity. Cilia contain various odorant receptors to which odorants bind and propagate a signal to the central nervous system (CNS), where the sense of smell is perceived. OSNs are unique neurons in that they both directly contact the external environment and the brain. While this direct contact allows OSNs to detect odors, it also makes them susceptible to environmental toxins leading to cell death. Upon their death, OSNs are replenished by basal stem cells in the OE leading to constitutive regeneration and neurogenesis. However, several forms of olfactory dysfunction can arise from various perturbations of OSNs, including disruption of olfactory cilia, cell death, or odorant signal transduction pathways. Some olfactory disturbances are treatable but more severe dysfunctions lack therapeutic remedies. In order to develop novel treatments for olfactory dysfunction, understanding the mechanisms of OE maintenance and uncovering additional etiologies of olfactory dysfunction are imperative. Many questions concerning the maintenance of the OE remain unanswered, including the



precise mechanisms and signaling pathways necessary for the cell division, cell fate, and cell differentiation of the basal stem cells. Various signaling pathways, including the cilia-dependent Hedgehog (HH) pathway, play important roles in adult stem cell function. In this chapter, I review: 1) the olfactory system itself, 2) the role of cilia in olfactory function, and 3) the role of cilia-dependent HH signaling as a potential novel regulator of olfactory maintenance and regeneration.

## **1.2 Olfaction: An Evolutionarily Conserved Sense**

### **1.2.1 Importance and Mechanism of Smell**

Olfaction, or the sense of smell, is an evolutionarily and historically important function. The importance of smell ranges across species and extends to prehistoric times. In early medicine, odor and taste were used often as a diagnosis of disease and for animals and prehistoric humans, olfaction was and remains important for survival in obtaining food, finding a mate, and avoiding predators (Doty, 2015). From ancient civilization to present-day, smell has been a large part of the quality of life of humans through the use of fragrances in religious rites and celebrations, as well as for skin care and food (Doty, 2015). In mammals, olfaction has been linked to behaviors related to alarm, feeding, mating, predator-prey relationships, social status appraisal, and species recognition through the social and emotional associations of certain smells (Doty, 2015). A major advance has been the discovery that the loss of smell is the first, or among the first, sign of common neurodegenerative diseases like Alzheimer's disease and Parkinson's disease (Doty, 2003a; Smutzer et al., 2003; Doty, 2015), making olfactory

testing an important early indicator of some neurodegenerative disorders. Olfaction has varying uses and levels of importance across species and this is due in part to the evolution of smell.

### *Evolution of Smell*

Olfaction began in an aquatic environment in which fish detected water-soluble odorants and evolved to incorporate both water-soluble and volatile odorants in four-limbed animals due to their dual environments on land and in water (Hoover, 2010). Eventually mammals evolved, and unlike other non-mammal vertebrates, used an organ, the nose, to detect volatile odors. Within the nose are nasal turbinates that help push odorants within the inhaled air into the olfactory epithelium (OE) via the orthonasal route (Shepherd, 2004). In humans, odorants also reach the OE via the retronasal route from the back of the oral cavity through the nasopharynx, allowing for smell perception of foods and liquids (Shepherd, 2004). Further evolution of humans was characterized by the increasing importance of other senses, like vision, due to the adoption of an erect posture which moved the nose away from the ground and closer to the face, allowing for the eyes to have more depth perception (Sarafoleanu et al., 2009). Although other senses have become important for humans, the sense of smell has not become irrelevant, but its importance has become associated with aspects that diverge from other mammals.

The basic organization of the olfactory system of humans and mice is similar with only some differences in its structure, making experimental information about the function of the mouse olfactory system applicable to humans (Harkema et al., 2012). A schematic of the mouse olfactory turbinates and resulting coronal sections can be seen in Fig. 1-1. From rodents to humans, there is a reduction in the proportion of functional odorant

receptor (OR) genes to total OR genes. In mammals, volatile odors are detected via ORs found in specialized primary cilia (small organelles important for cell function) that project from olfactory sensory neurons (OSNs) in the OE. While mice have approximately 1,300 – 1,500 OR genes with 1,100 that are functional (Young et al., 2002; Zhang and Firestein, 2002), humans only have 350 functional OR genes of the approximate 1,000 in the genome (Glusman et al., 2001). However, this reduction in humans is compensated by the larger capacity of human brain processing via the integration of various areas of olfactory perception in the brain (Sarafoleanu et al., 2009). This combination of odor detection in the main olfactory system and odor perception in the cerebrum is the basis for olfactory transduction.

### *Olfactory Transduction*

The main olfactory system detects odorants in the nasal cavity via OSNs and the resulting information is sent to various regions of the CNS. OSNs are bipolar neurons with a single dendrite that projects to the surface of the OE and ends in a structure called the dendritic knob. Basal bodies within the dendritic knob project cilia towards the nasal cavity into mucous of the OE. The human OE contains approximately 50 million OSNs with 8-20 cilia (Sarafoleanu et al., 2009) compared to 6-10 million OSNs in the mouse OE (Firestein, 2001). In most mammals and humans, lengths of OSN cilia are approximately 50µm, while in non-mammalian vertebrates such as frogs, they can be as long as 200µm (Menco and Morrison, 2003). These cilia are enriched in ORs and other signaling components that mediate the initial transduction events in the cell (Firestein, 2001). The family of ORs was initially identified as a large multigene family of olfactory-specific G protein-coupled receptors (GPCRs) in the rat (Buck and Axel, 1991). They exhibit

extensive sequence diversity within their transmembrane domains (the presumed ligand binding sites), allowing for the detection of a wide range of chemicals in the environment (DeMaria and Ngai, 2010). In addition to the ORs, a second family of receptors called trace amine-associated receptor (TAAR) family are also expressed in a unique subset of OSNs and are thought to recognize volatile amines (Liberles and Buck, 2006). The receptors within the multitude of OSN cilia increase the sensory surface area of the OE, priming the olfactory system for signal detection.

The signaling cascade for the sense of smell starts with the binding of an odorant to its receptor (Fig. 1-2A). Only volatile materials that are soluble in the mucous and that interact with specific OSNs produce odors (Turin and Yoshii, 2003). Odorant molecules pass through the nasal cavity, dissolve in the mucous and bind to their corresponding olfactory receptors. Upon odorant binding, the activated OR couples through the G-protein,  $G_{\alpha_{olf}}$ , which is a  $G_{\alpha_s}$  isoform enriched in OSNs (Belluscio et al., 1998). Activated  $G_{\alpha_{olf}}$  then activates type III adenylyl cyclase (ACIII) (Wong et al., 2000), which catalyzes the production of cyclic AMP (cAMP) (Fig. 1-2A). The increase in intracellular cAMP opens a cyclic nucleotide-gated (CNG) channel (Brunet et al., 1996), leading to an influx of sodium and calcium ions, and depolarization of the neuron (Fig. 1-2A). The initial depolarization is further amplified by the subsequent activation of calcium-activated chloride channels and, due to the low concentration of extracellular  $Cl^-$  in the mucus, the efflux of  $Cl^-$  from the cell (Stephan et al., 2009) (Fig. 1-2A). The odor-induced depolarization in the olfactory cilia spreads throughout the neuron, resulting in the opening of voltage-sensitive ion channels in the sensory neuron's axon hillock, the firing

of action potentials, and the release of neurotransmitter at the synaptic terminal (DeMaria and Ngai, 2010).

At the other end of OSNs, a single, unbranched axon projects to the olfactory bulb (OB), a structure in the forebrain that serves as the first relay of olfactory information. The axons of OSNs in the periphery together comprise the olfactory nerve (the first cranial nerve). Once the axons reach the OB, they form synapses with the dendrites of projection neurons within discrete structures known as glomeruli (DeMaria and Ngai, 2010) (Fig. 1-2B). Each OSN in the OE expresses just one allele of a single OR (Chess et al., 1994; Serizawa et al., 2003) – known as the “one receptor, one neuron” rule (DeMaria and Ngai, 2010). Although OSNs expressing a given OR are distributed broadly throughout the OE, their axons converge to specific glomeruli in the OB in a spatially invariant pattern (Ressler et al., 1993; Vassar et al., 1993; Ressler et al., 1994; Vassar et al., 1994; Mombaerts et al., 1996). The projection neurons of the OB, the mitral and tufted cells, extend their axons to the olfactory cortex which is comprised of several anatomically distinct areas including the piriform cortex, olfactory tubercle, anterior olfactory nucleus, and specific parts of the amygdala and entorhinal cortex (Zou et al., 2001) (Fig. 1-2C). Communication with the limbic system allows for interplay between smell and various processes like taste, memory and behavior.

### 1.2.2 Development and Anatomy of the Olfactory Periphery

The sensory organs of the vertebrate head derive from the sensory placodes and the cranial neural crest (NC) during embryogenesis. Placodes are discrete areas of thickened non-neural epithelium that give rise to the paired sensory organs including the olfactory system (Kato et al., 2011). The olfactory organ has been shown to arise from

a combination of the olfactory placode and cranial NC cells (Katoh et al., 2011). The role of the olfactory placode in olfactory development was first experimentally demonstrated in amphibians when obstruction of the olfactory placode disrupted the development of the OB (Burr, 1916). The importance of NC cells in the development of the olfactory system was demonstrated in rats with a mutation in the *Pax6* gene in which impaired migration of midbrain crest cells into the frontonasal mass led to the loss of the nasal placode (Osumi-Yamashita et al., 1997). Olfactory progenitors are believed to arise from the placode (Chuah et al., 2003) but some studies have revealed they might also arise from the NC (Katoh et al., 2011).

During development, neural stem cells are important for early neurogenesis and morphogenesis of the OE (Gokoffski et al., 2010). Apical and basal progenitors divide and differentiate into various cells resulting in a pseudostratified epithelium of five basic cell types (Chuah et al., 2003; Murdoch and Roskams, 2007). These cell types are morphologically and biochemically distinguishable. From the apical surface down, sustentacular (SUS) cells, mature and immature olfactory sensory neurons (OSNs), Bowman's gland (BG) duct cells, globose basal cells (GBCs), and horizontal basal cells (HBCs) make up the OE (Fig. 1-3). In addition to the five basic cell types, microvillar cells (MVCs) have also been observed in the OE (Moran et al., 1982; Morrison and Costanzo, 1990; Miller et al., 1995). In human and other mammalian embryos, there is a dramatic increase in mitosis in the OE immediately before the first emergence of olfactory axons at stage 13 (28 days) (Chuah et al., 2003). At this stage in development, mitosis in the OE is similar to the cell division observed in the developing neural tube (Chuah et al., 2003). The epithelial cells undergo interkinetic nuclear migration (Sauer, 1937) as G1-

and S-phases take place in deeper parts of the epithelium, and the cells migrate superficially to complete mitosis at the apical epithelial surface (homologous to the ventricular surface of the neural tube) (Smart, 1971; Chuah et al., 2003). Later in development, once the basal cell layer is established, a shift of mitotic activity occurs to the base of the OE (Smart, 1971; Chuah et al., 2003). The precise relationship between the apical and basal progenitor populations has not been clarified but neurons are being generated even at times when mitoses are concentrated apically (Chuah et al., 2003).

The most detailed studies on the development of the various cell types in the OE have been done in rodents. In mice, the OE begins to form at embryonic day 10 (E10), which is shortly after the placode begins to invaginate (Cuschieri and Bannister, 1975; Cau et al., 2000; Murdoch and Roskams, 2007). Within the olfactory placode, the order and progression of pro-neural genes that regulate olfactory neurogenesis have been revealed by genetic analysis of basic helix-loop-helix (bHLH) family proteins which are expressed in GBCs (Guillemot et al., 1993; Cau et al., 1997; Cau et al., 2002). This genetic analysis has led to the current model in which a pool of rapidly proliferating transit amplifying cells expressing *Ascl1* (formerly *Mash1*) give rise to *Ngn1*- and *NeuroD*-positive immediate neuronal precursors (Duggan et al., 2008). While maturing GBCs that migrate from the apical surface clearly contribute to organogenesis (Cau et al., 2002), the precise role of HBCs is unclear. Small numbers of p63-expressing cells, which are thought to be HBC precursors, first appear at E14, after the emergence of all other cell types (Packard et al., 2011b). HBCs settle to the basal lamina, begin to express Keratin5 (K5), and become dormant between ~E16 and P10 (Packard et al., 2011b). Due to their late emergence, HBCs are not believed to participate in the establishment of the OE.

However, evidence from a lineage-trace mouse model suggests that upon their establishment in the OE at postnatal day 10 (P10), HBCs do participate in neurogenesis to a lesser extent (Iwai et al., 2008).

The first cells to differentiate are neurons and slightly later, there is a major transition in the appearance of the epithelium, which coincides with the shift of mitotic activity from the apical epithelium to the basal region (Chuah et al., 2003). At this time, the various cell types become morphologically distinct (Chuah et al., 2003). The OE is separated from the lamina propria (LP), the underlying region, by a basement membrane called the basal lamina (Fig. 1-3A). The developing LP contains olfactory ensheathing cell (OEC) precursors and immature OECs which ensheath OSN axons (Murdoch and Roskams, 2007). The postnatal LP contains axon bundles, OECs, connective tissue, blood vessels, and Bowman's glands (Murdoch and Roskams, 2007). The highly vascularized LP is supplied by the ethmoidal artery which is distinct from sphenopalatine supply of the respiratory mucosa (Ding and Xie, 2015a). The resulting high perfusion rates in nasal tissue allow for rapid absorption and systemic distribution of substances that penetrate the OE, however, this high perfusion can also allow for toxins in the bloodstream to come in contact with xenobiotic-metabolizing enzymes in the olfactory mucosa (Ding and Xie, 2015b).

## OSNs

OSNs make up 80-85% of the epithelial cells and are densest in the posterior dorsal part of the OE (Menco and Morrison, 2003). They are comprised of mature and immature sensory neurons. Mature OSNs are identified by their expression of olfactory marker protein (OMP) (Danciger et al., 1989), and just below and blending in with the



basal cells are the immature OSNs identified by the expression of GAP43 (Verhaagen et al., 1989) and  $\beta$ -tubulin type III (Roskams et al., 1998).

### *SUS cells*

The supporting cells of the OE, SUS cells, make up 12-15% of the epithelial cells and span the apical olfactory epithelium tapering basally where they attach by foot-like processes known as endfeet to the basal lamina (Menco and Morrison, 2003) and make contacts with basal stem cells (Joiner et al., 2015). They are identified by a number of antigens including SUS1 (Hempstead and Morgan, 1983) and SUS4 (Goldstein and Schwob, 1996), as well as more defined markers like keratin 18, E-cadherin (Packard et al., 2011a), and transcription factors like Sox2 and Pax6 (Guo et al., 2010; Packard et al., 2011b). SUS cells are covered with microvilli that extend into the mucus and intermingle with olfactory cilia (Menco and Morrison, 2003). They are phagocytic and like CNS glia, provide structural support (Dennis et al., 2015). The SUS cells make multiple contacts with the OSNs and may release materials in and/or absorb material from the mucus (Menco and Morrison, 2003). They express high levels of enzymes known to participate in metabolic modification of toxicants, suggesting a glia-like protective role of the neuronal environment (Dennis et al., 2015). Some of these enzymes that SUS cells express include several cytochrome P450 isoforms (Ling et al., 2004) and glutathione S-transferase (GST) (Weech et al., 2003; Whitby-Logan et al., 2004).

The Notch receptor, a component of the Notch pathway that is involved in a variety of cell fate decisions during development, is expressed in adult glia (Rodriguez et al., 2008) and in the OE, while *Notch1* is known to be expressed in basal cells, *Notch2* (Carson et al., 2006; Rodriguez et al., 2008) and *Notch3* (Rodriguez et al., 2008), are

expressed in SUS cells. Studies have suggested that maintained expression of *Notch* receptors may be required to permanently establish fate in a differentiated cell type and that transient activation of the *Notch* pathway is sufficient to promote gliogenesis (Morrison et al., 2000; Tanigaki et al., 2001). One study investigated the role of *Notch* in SUS cells and found that the loss of *Notch2* leads to a decrease in expression of *P450s* and *GST*, as well as GST activity, that is accompanied by neurodegeneration of OSNs (Rodriguez et al., 2008). These findings support the idea of SUS cells having a neuroprotective role in the OE and show that *Notch* is important for this role.

#### *BG cells*

Like SUS cells, BG cells, are involved in metabolism of xenobiotic compounds (Ding and Dahl, 2003). The acinar and duct cells of BGs contain many xenobiotic-metabolizing enzymes but their localization is species dependent (Ding and Xie, 2015a). BGs found in the LP are responsible for the mucous secretion at the epithelial surface and the glands along with their duct complex, which enters the OE, allows for the olfactory cilia to be embedded in mucous (Menco and Morrison, 2003).

#### *MVCs*

There is approximately one MVC per SUS cell in the OE, making up about 1% of the olfactory epithelial cells (Miller et al., 1995). They have neuron-like morphology and are observed in the apical part of the OE (Dennis et al., 2015). Although their function and cell-lineage is unknown, there have been several studies that attempt to address the identity and role of MVCs in the OE. Multiple types of MVCs have been observed in the OE, including 1) microvillous OSNs with an axon projecting to the OB (Moran et al., 1982)

displaying a morphology similar to that of the microvillous sensory neurons found in the vomeronasal organ that express transient receptor channel C2 (TRP C2) (Liman et al., 1999) and 2) microvillous non-OSNs that lack a basal process or axon (Carr et al., 1991). Within the non-neuronal microvillous cell populations, a subset express the TRP M5 channel (Lin et al., 2007; Hansen and Finger, 2008) or phospholipase C beta-2 (PLC $\beta$ 2), TRP C6 and the type 3 inositol triphosphate receptor (IP3R3) (Elsaesser et al., 2005). A study that looked at the TRP5-expressing MVCs found that these cells also express choline acetyltransferase and are able to synthesize and potentially release Ach which modulates activities of OSNs and SUS cells (Ogura et al., 2011). Additionally, a study that focused on IP3R3-expressing MVCs found that these cells make contacts with nerve fibers and a subset are responsive to ATP, substance P and some odorants (Hegg et al., 2010). However, they do not possess neuronal or glial markers and do not project processes to the OB (Hegg et al., 2010). These findings suggest that IP3R3 MVCs might be a type of solitary chemosensory cell which respond to odorants at concentrations classified as irritants and may transfer sensory information via the nerve fibers (Hegg et al., 2010). These cells were also found to be a possible regulatory link between degenerating OSNs and olfactory stem cells (Jia and Hegg, 2012). Additional studies need to be performed to reveal the true classification and roles of MVCs.

### *GBCs and HBCs*

The GBCs and HBCs are the stem/progenitor cell populations of the OE and make up approximately 5% of the epithelial cells. GBCs are a heterogeneous population of actively cycling cells (Jang et al., 2014), while HBCs are a relatively homogeneous population of quiescent cells (Holbrook et al., 1995; Carter et al., 2004). HBCs resemble

the basal cells of the adjacent respiratory epithelium and envelop the olfactory axons as they exit the OE (Mackay-Sim, 2003). They are identified by their expression of a variety of antigens including keratins 5 and 14 and ICAM-1 (Holbrook et al., 1995). GBCs are round cells located more superficially than HBCs that are not seen in the respiratory epithelium (Goldstein and Schwob, 1996). A type of GBC that is located above the HBC layer but extends a slender process to contact the basal lamina has been interpreted as an intermediate form between HBCs and GBCs (Graziadei and Graziadei, 1979; Holbrook et al., 1995). The functions of HBCs and GBCs will be addressed in greater detail in the next section of this chapter. Together, these cells are important for the olfactory system to properly function.

### 1.2.3 Olfactory Dysfunction

Olfactory disorders arise from various disturbances, having a large impact on one's quality of life. They can be classified as (i) *anosmia* (absence of smell), (ii) *partial anosmia* (ability to perceive some odorants), (iii) *hyposmia* (decreased sensitivity to odorants), (iv) *hyperosmia* (abnormally acute olfactory function), (v) *dysosmia* (distorted smell perception), (vi) *phantosmia* (sensation in absence of odor stimulus) and (vii) *presbyosmia* (absence of smell due to aging) (Murphy et al., 2003). These impairments can occur from (i) nasal passage obstruction, (ii) damage to the OE and/or (iii) damage to the central nervous system (Murphy et al., 2003).

There are numerous reported etiologies for olfactory disturbance including various drugs, endocrine or metabolic disorders, industrial debris, viral and bacterial infections, lesions of the nose or airway blockage, neoplasms, neurological disorders, nutritional or metabolic imbalances, psychiatric disorders, and pulmonary diseases (Murphy et al.,

2003). Additionally, a normal decline in olfactory function due to aging afflicts approximately 25% of the population over 65 years old and this estimation is largely underrepresented (Murphy et al., 2002). If sensory information cannot be properly detected in the OE, transduced in the OB, or processed in the cerebrum, olfactory disturbances will occur.

### *Disturbance to OSNs*

Impairments to the OE are often associated with a loss of OSNs. Due to the contact of OSNs with damaging agents in the inhaled air, the olfactory system is vulnerable to insult. There are some defense mechanisms that the system employs in order to counteract this vulnerability. These mechanisms include 1) the detection of irritants by the nerve endings of the trigeminal nerve to trigger a flight response and change in breathing rate and/or pattern to minimize the entry of the irritant into the airways (Hastings and Miller, 2003) and 2) the metabolism of these xenobiotics through the presence of phase I and phase II enzymes – cytochrome P450s, glutathione, and related enzymes (Reed, 1993). However, these protective systems can fail and result in olfactory deficits after some toxic exposures (Hastings and Miller, 2003). Exposure to various compounds at certain concentrations can affect the histology and function of specific cells in the OE (for review, see ref. Hastings and Miller, 2003). Additionally, there is a net loss of OSNs over time due to the fact that the capacity to match OSN death with regeneration is compromised as a function of age (Conley et al., 2003). This compromise can be attributed to the dramatic decrease in basal stem cell proliferation with age, with olfactory cell proliferation decreasing ~10 to 15 times after birth during the first 3 months of life (Legrier et al., 2001; Ducray et al., 2002). Upper respiratory infections can also lead to

loss of OSNs, a decrease in OSN cilia, and respiratory infiltration (Murphy et al., 2003), which ultimately lead to olfactory dysfunction.

### *Disturbance to Signaling Machinery*

Disturbances to smell can also be associated with dysfunction in the signaling machinery of OSNs. Channelopathies, a class of disorders that are associated with mutations in genes that encode ion channel subunits or regulatory proteins (Kass, 2005) are associated with olfactory disturbances. Mice that lack the potassium channel,  $K_v1.3$ , were shown to be “super-smellers” with increased discrimination of odor molecules and increased odor threshold (Fadool et al., 2004; Biju et al., 2008). This phenotype is most likely associated with the altered axonal targeting of OSNs exhibited in  $K_v1.3$ -null mice (Biju et al., 2008). Additionally, the loss of the sodium channel,  $Na_v1.7$ , in mice led to a decrease in odor-guided behaviors, odor discrimination, and innate avoidance towards predator odor (Weiss et al., 2011). The OSNs in these  $Na_v1.7$ -null mice still evoke action potentials but fail to initiate synaptic signaling to the projection neurons in the OB (Weiss et al., 2011). A more recent manifestation of diseases related to olfactory dysfunction is the group of disorders associated with a dysfunction in cilia, termed ciliopathies, which will be discussed in greater detail later in this chapter.

### *Blockage and Disturbance to the CNS*

Nasal and sinus disease as well as intranasal and intracranial tumors can obstruct the nasal cavity leading to blockage of airflow or disturbance to the CNS resulting in a loss of olfaction (Murphy et al., 2003). Also, some viruses can infiltrate the CNS and influence central structures independent of peripheral damage (Baker and Genter, 2003).

Psychiatric disorders such as schizophrenia and chronic hallucinatory psychoses are associated with altered olfactory function affecting the CNS (Smutzer et al., 2003). Head trauma can cause olfactory dysfunction and the likelihood of anosmia is dependent on the severity of the injury (Costanzo et al., 2003). Traumatic olfactory dysfunction may be caused by: 1) sinonasal contusions or fractures without direct damage to the olfactory apparatus, 2) tearing or shearing of olfactory nerve filaments, or 3) contusion or hemorrhage within the olfactory-related brain regions (Costanzo et al., 2003).

### *Current Therapies*

Meaningful treatments are available for some, but not all, patients with an olfactory disturbance. The prognosis for patients suffering from long-standing total loss of smell due to upper respiratory illness or head trauma is poor. There are, however, several treatments and surgical procedures to help the improvement of smell, but the prognosis for recovery seems to be better for patients with less severe olfactory dysfunction (Murphy et al., 2003). For loss of smell due to obstruction of the airway, surgery and steroid therapy can reduce the obstruction and improve the sense of smell (Murphy et al., 2003). However, there is no current treatment for congenital olfactory dysfunction or loss of smell due to malformations of the olfactory bulbs and stalks (Murphy et al., 2003). In general, olfactory dysfunction due to sensorineural causes such as upper respiratory illness or head trauma is difficult to treat. Prognosis for recovery appears to be better for patients with less severe hyposmia than for those with anosmia, which may reflect the less extensive damage into the basal layer of the epithelia and possibly less fibrosis around the cribriform plate through which the olfactory nerves pass (Murphy et al., 2003). The use of basal stem and progenitor cells as a viable therapeutic strategy has been proposed

but is still in very early stages of investigation (Krolewski et al., 2011). Furthermore, a more complete understanding of olfactory stem cell function could aid in the development of future therapies.

## **1.3 Adult Neurogenesis**

### **1.3.1 Distinct Areas of Adult Neurogenesis**

Stem cells have varying potencies and capabilities ranging from totipotent stem cells that can give rise to a full organism, to pluripotent stem cells that can give rise to every cell of the organism except the trophoblasts of the placenta, to multipotent stem cells that are believed to give rise to only cells of the organ from which they are derived (Gage, 2000). Neurogenesis occurs from the self-renewal and differentiation of neural stem cells (NSCs), which can give rise to cells other than themselves through asymmetric cell division (Gage, 2000). NSCs exist in the developing and adult nervous system of all mammalian organisms, however, areas of continuous adult neurogenesis have been identified in the olfactory epithelium (OE), the subventricular zone (SVZ) of the lateral ventricle, and the subgranular zone (SGZ) of the hippocampus (Altman and Das, 1965; Gage, 2000; Alvarez-Buylla and Garcia-Verdugo, 2002; Lie et al., 2004).

In the adult OB, neural stem cells in the SVZ, a layer of dividing cells located along the lateral wall of the lateral ventricles, proliferate and give rise to neuroblasts which then migrate in the rostral migratory pathway and differentiate into granule and periglomerular neurons (Doetsch, 2003; Lie et al., 2004). There are four main cell types in the SVZ; neuroblasts, astrocytes, immature precursors, and ependymal cells (Doetsch et al.,



1997). The dominant cell in the rodent SVZ is the dual-functioning astrocyte which can serve as both a neural stem cell (NSC) and a supporting cell that interacts with other astrocytes to promote neurogenesis (Lim and Alvarez-Buylla, 1999).

In the adult hippocampus, neural progenitors located in the SGZ, a germinal layer in the hippocampus located between the granule cell layer and hilus of the dentate gyrus, proliferate and give rise to dentate gyrus granular neurons (Doetsch, 2003; Lie et al., 2004). Foci within the SGZ contain astrocytes, which extend basal processes under the blades of the dentate gyrus and an apical process into the granule cell layer and dividing immature Type D cells, which express markers for neuronal differentiation, newly generated neurons, and endothelial cells (Palmer et al., 2000; Seri et al., 2001). As in the SVZ, SGZ astrocytes are the primary precursors of neurons and divide to generate granule neurons via Type D cells (Seri et al., 2001).

Various studies suggest that factors and mechanisms that regulate proliferation, migration, differentiation, and cell survival during development are reactivated in the injured adult environment, allowing for tissue repair and neuroplasticity (Lie et al., 2004). Transplantation studies suggest that adult neural stem/progenitor cells from different regions are not fate-restricted by intrinsic programs but by extrinsic cues derived from the local environment (Lie et al., 2004). The adult olfactory system is an example of extraordinary plasticity in its ability to respond to injury through the replacement of neurons by olfactory stem cells (Joel, 2003).

### 1.3.2 Constitutive Neurogenesis in the Olfactory Periphery

Early evidence that OSNs could regenerate after damage was seen in primates in 1960 (Schultz, 1960). Studies have shown that the type of repair seems to correlate to the degree or extent of initial damage (Mackay-Sim, 2003). The discovery of the co-existence of mitotic cells, immature sensory cells, mature sensory cells, and dying cells suggested that sensory cells are continually replaced (reviewed in Mackay-Sim, 2003). This hypothesis was further supported by other investigators proving that the OE is a system of renewal and regeneration (Graziadei and Graziadei, 1979; Graziadei and Monti Graziadei, 1983). This survival process allows olfactory function to continue throughout the lifetime of an organism. In the mouse, this neurogenesis occurs during three phases: embryonic establishment (E10-P0), postnatal expansion (P1-P30), and postnatal maintenance (P30-death) (Murdoch and Roskams, 2007).

#### *GBCs and HBCs*

The precise mechanisms controlling regeneration and homeostasis in the OE are unclear; however, there are several proposed models. Regeneration and neurogenesis is thought to occur through the differentiation of GBCs, HBCs, or a combination of both (Graziadei and Graziadei, 1979; Calof and Chikaraishi, 1989; Leung et al., 2007; Iwai et al., 2008; Jang et al., 2014), but there still remains controversy over which cell type is the true stem cell population. GBCs are neurogenic and bi-potential since they can produce both OSNs and SUS cells (Murdoch and Roskams, 2007). Several studies show that GBCs are neuronal precursors that exist as a heterogeneous population, compartmentalized by their expression of distinct transcription factors. In the GBC lineage cascade, *Ascl1* (*Mash1*) expression lies upstream of *Neurogenin1* (*Ngn1*) which lies upstream of, but also overlaps with, *NeuroD1* expression (Cau et al., 1997; Manglapus et

al., 2004; Packard et al., 2011a; Krolewski et al., 2013). *NeuroD1* is eventually switched off prior to the onset of postmitotic differentiation, and low levels of *NeuroD1* are sometimes found in immature OSNs (Packard et al., 2011a). HBCs are multipotent progenitors with a more quiescent “stem-cell” like behavior (Murdoch and Roskams, 2007). The transcription factor, p63, was found to be a regulator of HBC dormancy and activation and is highly expressed in the basal cell layer of skin and other stratified epithelia (Packard et al., 2011b). Additionally, the basal cell cytokeratins K5/K14 which mediate adhesion to the basal lamina and in the OE are distinctly expressed in HBCs (Holbrook et al., 1995) and are among the genes directly regulated by p63 (Packard et al., 2011a). When p63 is downregulated, HBCs are thought to be activated (Packard et al., 2011a) and can differentiate into GBCs (Leung et al., 2007), suggesting that they are GBC precursors and replenish the GBC population upon damage.

#### *Other Possible Stem Cells*

In addition to the basal cells of the OE, the human olfactory mucosa contains a stem cell known as an “ectomesenchymal” stem cell with properties of mesenchymal and neural stem cells (Delorme et al., 2010). It is grown *in vitro* from whole mucosa which includes cells of the OE and LP and has the capability of differentiating into neurons, astrocytes, oligodendrocytes, and non-neural cell types such as cardiac and skeletal muscle, chondrocytes, osteocytes, liver cells, and fat cells (Murrell et al., 2005; Murrell et al., 2008; Delorme et al., 2010; Wetzig et al., 2011). It is possible that the ectomesenchymal stem cell in the adult olfactory mucosa is derived from the ectomesenchymal stem cell that migrates out from the cranial neural crest during

embryogenesis which give rise to multiple neural and non-neural tissues of the head (Mackay-Sim et al., 2015).

### *Lesion Models*

In order to study the restoration of the OE, transgenic mouse models are used to study the lineage of cells as they divide and differentiate into various cell types in the OE. Particularly, the use of Cre-Lox fate mapping to track genetic lineage of gene expression with lesion models of the OE has uncovered some insight to this restoration (Murdoch and Roskams, 2007). The main lesion models used include a surgical bulbectomy and a chemical/pharmacological lesion.

A bulbectomy is the removal of the OB, which in rodents induces a retrograde wave of apoptosis in OSNs within 24-36 hours of lesion (Cowan and Roskams, 2004). This apoptosis stimulates mitosis in local progenitors and OSNs are generated from adult OE-residing progenitors, with a rapid increase in the number of immature OSNs by 10 days and a return of mature OSNs by 3 weeks (Verhaagen et al., 1990). This lesion model limits axon-retargeting and allows the analysis of OSN regeneration only (Schwob et al., 1992). A chemical/pharmacological lesion leaves the OB available for retargeting, but destroys multiple cell types. Tritonx100, ZnSO<sub>4</sub>, MeBr gas and the thyroid drug methimazole are effective in inducing widespread OE cell loss and stimulating regeneration of multiple lineages (Harding et al., 1978; Schwob et al., 1995; Bergman and Brittebo, 1999). If damage is too severe, regeneration can be incomplete or respiratory epithelium can replace the OE (Jang et al., 2003) (Xie et al., 2010). After MeBr treatment, proliferation initially occurs at 1-2 days, peaks at 1 week and continues for up to 4 weeks with the OE almost fully restored by 6 weeks (Murdoch and Roskams, 2007).

Methimazole (MMI) is currently used over the more toxic MeBr and works by binding to SUS and BG cells, causing OE destruction via the formation of toxic metabolites mediated by P450s (Brittebo, 1995; Bergman et al., 2002), depleting the GBCs and sparing the HBCs in the mouse OE (Brittebo, 1995; Packard et al., 2011b).

Evidence from these lesion models so far has shown that GBCs frequently divide and, during neuronal-specific lesions, are the lead contributor to replacing OSNs through differentiation (Caggiano et al., 1994; Huard et al., 1998) (Fig. 1-4A-B). However, evidence has also shown that when there is a severe lesion that results in the death of not only OSNs, but SUS cells and often GBCs, HBCs, which are the more quiescent cell population, become proliferative and differentiate into multiple cell types to regenerate the OE (Carter et al., 2004; Leung et al., 2007; Iwai et al., 2008) (Fig. 1-4A, C). Within 18 hours of unilateral MeBr exposure, *p63* levels in HBCs are reduced in the lesioned side of the OE compared to unlesioned side and during the next day, some HBCs proliferate and lose all detectable *p63* expression while retaining keratins 5 and 14 and ICAM-1 expression (Schnittke et al., 2015). These data suggest that *p63* prevents the activation and multipotency of HBCs. During olfactory neurogenesis, GBCs go through the following stages, 1) multipotent stem cells (Chen et al., 2004), 2) multipotent progenitors that can generate multiple epithelial cells in response to injury (Huard et al., 1998) and express, 3) transit amplifying cells which are committed to neurons (Guillemot et al., 1993), and 4) immediate neuronal precursors which undergo a final division and differentiate into neurons (Calof and Chikaraishi, 1989; Cau et al., 1997). Following injury, residual GBCs express *Sox2* and *Pax6* (Guo et al., 2010), when the cells are considered to be multipotent stem cells, and then go on to express *Ascl1* (formerly known as *Mash1*), as

they become transit amplifying cells, then *Neurog1* and *NeuroD1* as followed by differentiation of post-mitotic daughter cells into immature OSNs (Cau et al., 1997; Manglapus et al., 2004). While some of the transcription factors that are turned off or on during the division and differentiation of HBCs and GBCs are known, the molecular regulation of these cells, including proliferation in response to injury and cell fate determination during differentiation, remains largely unexplored (Doty, 2003b; Manglapus et al., 2004).

### 1.3.3 Regulation of Olfactory Neurogenesis

Various regulatory factors are thought to regulate neurogenesis of the OE including positive regulator factors that sense a need for more OSNs and stimulate mitosis and differentiation and a reduction in negative feedback from mature OSNs to inhibit additional OSN production (reviewed in Murdoch and Roskams, 2007; Mackay-Sim et al., 2015). Positive regulators include the leukemia inhibitory factor (LIF), a mitogen that contributes to proliferation in embryonic and postnatal OE *in vitro* and *in vivo*, the fibroblast growth factor (FGF), transforming growth receptor  $\alpha$  (TGF $\alpha$ ), and epidermal growth factor (EGF), which binds to and signals through the EGF receptor, EGFR), and are most prominently expressed in HBCs and SUS cells (reviewed in Murdoch and Roskams, 2007). Factors that negatively regulate OSN genes include TGF- $\beta$  superfamily of growth factors made up of TGF- $\beta$ , activins, and BMPs (Murdoch and Roskams, 2007). These proteins are highly conserved and play active roles during differentiation and development of variety of tissues and signal via a serine-threonine kinase receptor complex (reviewed in Murdoch and Roskams, 2007). Additionally, increased BMP signaling can inhibit neurogenesis and was found to induce respiratory epithelial character at the expense of

sensory epithelial character during development (Maier et al., 2010). ATP and the peptide NPY were also shown to play a role in basal cell proliferation via SUS cells (Jia and Hegg, 2010).

The Notch and Wnt signaling pathways have also been proposed to play important roles in the neurogenesis of the OE. The Notch signaling pathway regulates cell proliferation, cell fate, differentiation, and cell death (Kopan, 2012). Notch is a cell-surface receptor that transduces short-range signals by interacting with transmembrane ligands (Kopan, 2012). In the olfactory system, Notch signaling is thought to play a key regulatory role in GBC differentiation (Manglapus et al., 2004). It is known to stimulate expression of Hes1 and Hes5, proteins seen in the GBCs of recovering olfactory epithelium, and *Notch* is expressed by some GBCs (Manglapus et al., 2004). The Wnt signaling pathway plays critical roles during embryonic development and in the regeneration of adult tissues and regulates cell fate determination, motility, polarity, and stem cell renewal (reviewed in Komiya and Habas, 2008; Rodriguez-Gil and Greer, 2008; Clevers and Nusse, 2012). Wnt proteins are secreted glycoproteins that bind to the extracellular domain of the Frizzled receptor to initiate signaling (Komiya and Habas, 2008). The pathway exists as a canonical pathway which is  $\beta$ -catenin-dependent and a non-canonical pathway which is  $\beta$ -catenin-independent (Komiya and Habas, 2008). Wnt signaling is important in adult stem cells of the intestine, skin and hematopoietic system (Grigoryan et al., 2008). In the OE, Wnt signaling was found to augment GBC proliferation and prevent transit amplifying neuronal progenitor cells from further differentiation into mature OSNs (Chen et al., 2014). Additionally, Wnt proteins were seen in the OECs in the LP and in adult glomeruli indicating a role in axonal guidance (Rodriguez-Gil and Greer, 2008). Although there have

been advances in olfactory research, there are still many unanswered questions, including the precise signaling involved in neurogenesis.

## **1.4 Cilia: Important Signaling Antennas**

### **1.4.1 Motile and Primary Cilia**

Cilia are specialized cellular compartments or organelles found in most mammalian cell types with varying important roles. Many unicellular organisms and some specialized vertebrate cells contain multiple, motile cilia which beat in a coordinated and polarized manner for locomotion, feeding, sensation, or to drive directional fluid flow across tissues (Brooks and Wallingford, 2014). In vertebrates, including humans, most cells possess or are capable of generating single, non-motile primary cilia, which serve as critical regulators of signal transduction during development and homeostasis (Brooks and Wallingford, 2014).

The primary cilium, which was first named by Sergei Sorokin (Sorokin, 1968) is a single, non-motile organelle that projects from the cell surface of most mammalian cell types during growth arrest (Satir et al., 2010). Primary cilia act as communication scaffolds to coordinate signaling pathways that are critical in embryonic and postnatal development as well as in adult tissue homeostasis (Pedersen et al., 2008). Signaling in cilia mediate key cellular processes including cell migration, differentiation, and/or re-entry into the cell cycle, specification of the plane of cell division, and apoptosis. Cilia respond to mechanical stimulation (bending of the cilium) and chemosensation (detection of a specific ligand, growth factor, hormone, or morphogen) (Satir et al., 2010).



## *Development and Maintenance of Cilia*

The assembly of primary cilia is tightly coupled to the cell cycle. It occurs from the distal end of the mother centriole as cells enter growth arrest and then sheds shortly before cells enter mitosis (Quarmby and Parker, 2005; Plotnikova et al., 2009). During interphase of the cell cycle, a modified centriole migrates to the plasma membrane and attaches to a Golgi-derived vesicle forming the basal body which templates the nucleation of the axoneme, the structural core of the cilium (Sorokin, 1968). The basal body is composed of 9 sets of microtubules and serves as the microtubule organizing center (MTOC) from which axonemal tubules project (Burton, 1992). These specialized structures result in various functions in the different cell types. Most motile cilia have an additional central microtubule pair resulting in a 9+2 configuration while primary cilia are usually immotile and lack a central pair resulting in a 9+0 configuration with the exception of primary motile cilia present on the embryonic node (Singla and Reiter, 2006). In contrast to those of motile 9+2 cilia, the axonemes of non-motile primary cilia lack key elements involved in ciliary motility, including the central pair of microtubules and the outer and inner dynein arms that power microtubule sliding to produce motility (Satir and Christensen, 2007).

Assembly of the axoneme is mediated by intraflagellar transport (IFT) (Pedersen et al., 2008). IFT was first described in the alga *Chlamydomonas reinhardtii* (Kozminski et al., 1993) and is essential for the construction and maintenance of cilia in all species (Singla and Reiter, 2006; Pedersen et al., 2008). Its basic mechanisms are widely conserved not only between cilia types but also often between species (Sung and Leroux, 2013). Since cilia lack the necessary components for protein synthesis, structural

components of the cilium and cargo must be synthesized in the cell and carried into cilia through the IFT system (McEwen et al., 2008). IFT is a bidirectional motility system localized between the outer doublet microtubules and the ciliary membrane by which particles are moved into and out of the cilium by molecular motors (Rosenbaum and Witman, 2002): 1) a kinesin motor responsible for anterograde transport toward the distal plus end of the cilium, and 2) a dynein motor that mediates retrograde transport of cargo out of the cilium and back into the cell (Hirokawa et al., 1998) (Fig. 1-5). Motors associate with 2 distinct complexes of IFT proteins: complexes A and B, which comprise a set of highly conserved proteins (Cole et al., 1998; Cole, 2003) (Fig. 1-5). Besides IFT complex proteins, there are a number of other proteins involved in cilia establishment, maintenance, and particle entry and movement. The BBSome (Loktev et al., 2008; Scheidecker et al., 2014) is a group of eight conserved proteins affected in human Bardet-Biedl syndrome (BBS) (Zaghloul and Katsanis, 2009), a pleiotropic disorder characterized by obesity, polydactyly, retinal dystrophy, and cystic kidneys. It is proposed to interact with IFT complexes and participate in particle entry and movement (Liew et al., 2014; Williams et al., 2014). When some of these ciliary proteins are defective, they are a major cause of human diseases and developmental disorders known as ciliopathies (Veland et al., 2009).

### *Growing Roles of Cilia and Disease*

Defects in cilia function lead to various human diseases, termed ciliopathies, which are a diverse class of congenital diseases with 23 recognized syndromes caused by mutations in at least 89 different genes (van Reeuwijk et al., 2011). These diseases are highly pleiotropic and the degree of penetrance can vary between patients (McIntyre et

al., 2013). Various impairments can occur including blindness, hearing loss, altered nociception, and anosmia as well as renal and liver cysts, airway distress, and hydrocephaly (reviewed in van Rееuwijk et al., 2011)

Evidence that dysfunction of non-motile cilia play a role in human disease was first considered after the orthologous protein of human polycystin-1 (PC1), which is mutated in autosomal dominant polycystic kidney disease (ADPKD) type 1, was shown to be expressed in ciliated neurons of *C. elegans* (Barr and Sternberg, 1999). Proteins of mutated genes in cystic kidney diseases were later found to localize to primary cilia, including the IFT protein IFT88/Polaris (Pazour et al., 2002b). The significance of primary cilia in signaling became clear upon examination of a hypomorphic mutant mouse, *Tg737<sup>orpkRpW</sup>*, which is deficient in the homolog of IFT88 (Lehman et al., 2008). The mouse was developed as a model for human autosomal recessive polycystic kidney disease (ARPKD) because they eventually developed polycystic kidneys. It was found that upon development of ARPKD in these mice, like other models of the disease, PC1, PC2 and the transient receptor potential (TRP) Ca<sup>2+</sup> channel protein complex were mislocalized or absent from primary cilia (Pazour et al., 2002a; Yoder et al., 2002). These mice were also later found to be anosmic (McIntyre et al., 2012). Another complex of recessive cystic kidney diseases is nephronophthisis (NPHP) which results from defects in the genes that encode for Nephrocystin (Nphp) 1-9 (reviewed in Veland et al., 2009). Other ciliopathies include Joubert syndrome in which mutations in *ARL13B* were found in patients (Cantagrel et al., 2008) and Meckel syndrome, in which mutations in *NPHP* were found (Craigie et al., 2010).

#### *Cilia and Olfactory Dysfunction*

Olfactory dysfunction due to ciliary defects can occur by 2 separate mechanisms: 1) a complete loss of olfactory cilia and 2) a defect in protein trafficking leading to a loss in olfactory signaling (McEwen et al., 2008). The first documented case of a human patient with anosmia presumably due to ciliary defects was in 1975 in which the patient had OSNs devoid of cilia (Douek et al., 1975). Since then, olfactory deficits were shown to occur in 2 different pleiotropic diseases, BBS and Leber Congenital Amaurosis (LCA). There have been observations that patients with BBS are frequently unable to smell (reviewed in Fliegauf et al., 2007). Mice that lack BBS1 or BBS4 have a severely reduced olfactory ciliated border and defects in the highly specialized ciliated dendritic knobs (Kulaga et al., 2004). Additionally mice that lack BBS8 also show decreased olfactory function (Tadenev et al., 2011). LCA is a congenital retinal dystrophy and can occur due to mutations in several proteins of varying function, including mutations in the centrosomal/basal body protein CEP290 (reviewed in McEwen et al., 2008). Mutations in CEP290 resulted in severely impaired olfactory function despite a self-described normal sense of smell which was due to mislocalization of G-proteins rendering the signaling pathway nonfunctional (McEwen et al., 2007).

#### 1.4.2 Cilia in Adult Neurogenesis and Tissue Homeostasis: Implications in Signaling Pathways

Recent research has shown a growing role for cilia in stem cell proliferation and differentiation. Primary cilia are required for the formation of adult neural stem cells in the hippocampal dentate gyrus during development, and also play an essential role in the initiation of mesenchymal stem cell differentiation (Tummala et al., 2010; Amador-Arjona et al., 2011). There is also evidence that human embryonic stem cells (hESCs) possess

primary cilia, which contain important components of the HH pathway (Kiprilov et al., 2008). Quiescent stem cells in the subventricular zone (SVZ) and the subgranular zone (SGZ) of the dentate gyrus were shown to arise in late embryonic stages and respond to SHH during their differentiation into various cell types (Ahn and Joyner, 2005). Additionally, primary cilia were found to be required for proper proliferation and neurogenesis in a specific subregion of the postnatal ventricular-SVZ as well as for proper HH signaling (Tong et al., 2014).

In regards to differentiation, cilia play important roles in various signaling pathways essential for proper cell differentiation during development and adult homeostasis. These pathways include Platelet-Derived Growth Factor (PDGF), Sonic Hedgehog (SHH) and Wnt (reviewed in Gerdes et al., 2009), which is important in adult stem cells of the intestine, skin and hematopoietic system (Grigoryan et al., 2008). In the adult skin, a loss of IFT88 from basal cells resulted in proliferation of cells in the interfollicular epidermis but not the follicle, and an overall abnormal differentiation in skin homeostasis (Croyle et al., 2011). Conversely, in the hippocampus, when cilia were removed postnatally from neural stem cells (NSCs) via genetic deletion of the IFT gene, *Ift20*, the number of neural stem cells (NSCs) remained the same in mutants compared to controls with an overall reduction in proliferation in the SVZ and a reduction in neurogenesis (Amador-Arjona et al., 2011). In the adult kidney of mice, loss of the kinesin motor, Kif3a, resulted in cyst formation and increased proliferation following an injury (Sharma et al., 2013).

Mice with defective IFT proteins and mutations in BBS genes exhibit phenotypes resembling those observed in mutants of the non-canonical Wnt pathway (reviewed in Goetz and Anderson, 2010), which is also known as the polar cell polarity (PCP)

pathway (Klein and Mlodzik, 2005). The primary cilium was proposed to act as a switch between canonical and non-canonical Wnt signaling pathways but the connection between cilia and Wnt signaling is controversial (Corbit et al., 2008; Huang and Schier, 2009). The PCP pathway is a conserved signaling pathway for coordinated polarization of cells within the plane of an epithelial cell layer (reviewed in Hildebrandt et al., 2011). Core planar cell polarity proteins are sorted asymmetrically along the polarization axis and the protein IFT88/Polaris is required for establishing epithelial planar cell polarity (Jones et al., 2008). Proper positioning of ciliary basal bodies and the formation of polarized cellular structures are disrupted in mice with mutant ciliary proteins (reviewed in Hildebrandt et al., 2011). The HH pathway, which will be discussed in greater detail in the next section of this chapter, has been implicated in the maintenance of stem/progenitor cells in many adult tissues (reviewed in Dessaud et al., 2008; Balbuena et al., 2011; Petrova and Joyner, 2014). Further investigation of these signaling pathways in the OE could answer many open questions pertaining to the regulatory signaling that occurs during neurogenesis and restoration of the OE.

## **1.5 The Hedgehog (HH) Signaling Pathway**

### **1.5.1 Canonical HH Signaling Mechanisms**

The Hedgehog (HH) signaling pathway is critical for normal embryonic development and plays important roles in adult tissue maintenance. HH was first discovered in a genetic screen aimed to understand the body segmentation of *Drosophila* (Nusslein-Volhard and Wieschaus, 1980), in which mutant embryos developed were

phenotypically reminiscent of a Hedgehog animal, due to the lack of segment boundaries. The core components of the HH pathway were also initially identified in *Drosophila* (Nakano et al., 1989; Alcedo et al., 1996) and are conserved in vertebrates (Echelard et al., 1993; Krauss et al., 1993; Riddle et al., 1993; Goodrich et al., 1996). The HH ligand is first synthesized as a 45kDa precursor that undergoes autocatalytic cleavage to generate a 19kDa processed form that is modified by the covalent attachment of a cholesterol molecule to the C-terminus (Porter et al., 1996) and addition of palmitate, a saturated fatty acid, (Chamoun et al., 2001) to the N-terminus in order to attain its final secreted form. In *Drosophila* and in mammals, the protein, Dispatched, is specifically required for the controlled release of the modified HH ligand (Burke et al., 1999). When HH is secreted, it acts in a concentration- and time-dependent manner to initiate various cell responses such as cell survival, proliferation, and cell fate specification and differentiation.

HH signal transduction is initiated at the plasma membrane of HH-responsive cells where it interacts with its 12 transmembrane protein receptor, Patched (Ptc in *Drosophila*; Ptch1 in vertebrates) (Chen and Struhl, 1996; Marigo et al., 1996; Stone et al., 1996) which is facilitated by the Ihog/Cdo family of co-receptors (McLellan et al., 2006; Tenzen et al., 2006; Yao et al., 2006). The binding of HH to Patched sequesters HH by internalizing the Patched/HH complex and targeting it to lysosomes for degradation (Gallet and Therond, 2005). This event also increases the expression and activation of Smoothed (Smo) (Chen and Struhl, 1996; Deneff et al., 2000; Ingham et al., 2000) via a conformational change (Fan et al., 2012) which results in the downstream signaling cascade that functions to regulate the HH transcription factors.

In mammals, there are three paralogues of HH genes (Echelard et al., 1993): Sonic HH (SHH, the most broadly expressed and best studied HH molecule), Indian HH (IHH, primarily involved in bone differentiation) and Desert HH (DHH, involved in gonad differentiation). Two major differences between HH signaling in *Drosophila* and vertebrates include: 1) while there is a single ancestral gene encoding the transcription factor, *Ci*, in *Drosophila*, three genes comprise this family (*Gli1*, *Gli2*, and *Gli3*) in vertebrates, and 2) the requirement in vertebrates for intraflagellar transport (IFT), which is necessary for the establishment and maintenance of cilia. The first indication of a potential role for cilia in mammalian HH signaling emerged from genetic screens in the mouse which identified mutations in IFT genes that produced patterning defects similar to those of mutations in genes encoding HH pathway components (Huangfu et al., 2003). Both PTCH1 and SMO can localize to primary cilia in a mutually exclusive way, where the binding of HH ligand to PTCH1 allows SMO to move into the cilium where it accumulates and promotes pathway activation through the HH transcription factors (Rohatgi et al., 2007) (Fig. 1-6). The transcription factors then undergo various processing events to either inhibit or activate the pathway (Fig. 1-6).

### 1.5.2 GLI Processing in HH Signaling

The GLI family of transcription factors mediates most vertebrate HH signaling and it is proposed that cilia are required for the differential regulation of these transcription factors (Casparly et al., 2007). GLI proteins localize to primary cilia and require intact IFT for proper processing and function (Haycraft et al., 2005; Liu et al., 2005). Disruption of the HH pathway results in aberrant cell growth, differentiation and migration with a tissue homeostatic imbalance leading to severe disorders (Mimeault and Batra, 2010). When



the IFT protein, IFT88, and cilia are disrupted, SMO translocation and GLI processing is perturbed, resulting in HH-specific phenotypes (Huangfu et al., 2003; Haycraft et al., 2005; Goetz and Anderson, 2010).

HH signaling results in a change in the balance between the activator and repressor forms of the Ci and GLI proteins by regulating their post-translational proteolytic processing (Fig. 1-7). All GLI and Ci proteins have a Zn-finger DNA-binding domain (Kinzler et al., 1988) and a C-terminal activation domain, while only Ci, GLI2 and GLI3 contain an N-terminal repressor domain (Sasaki et al., 1999; Briscoe and Therond, 2013) (Fig. 1-7). GLI1 has diverged evolutionarily, lacking a transcriptional repressor domain (Park et al., 2000). The post-translational regulation of Ci and GLI proteins is similar, however, each GLI protein has a unique role.

In *Drosophila*, in the absence of HH ligand, the C-terminal domain of Ci undergoes sequential phosphorylation on multiple sites, first by PKA and then by glycogen synthase kinase 3 $\beta$  (GSK3 $\beta$ ) and different members of the casein kinase I (CKI) family (reviewed in Hui and Angers, 2011). These events lead to the recruitment of an E3 ubiquitin ligase complex (Jia et al., 2005; Smelkinson and Kalderon, 2006) and ubiquitylation of specific residues targets the modified protein to the proteasome, where the C-terminal transactivation domain is removed by partial degradation (Briscoe and Therond, 2013). The remaining protein, which comprises the N-terminal repressor domain and DNA-binding domains, translocates to the nucleus, binds genomic target sites and represses transcription. In the presence of HH ligand, activation of SMO inhibits the phosphorylation and partial proteolytic processing of Ci, allowing full length Ci to act as a transcriptional activator.

In vertebrates, in the absence of HH ligand, GLI proteins are retained in the cytoplasm by the kinesin-4 protein, KIF7, and suppressor of fused, SUFU, to limit transcriptional activation (Kogerman et al., 1999; Merchant et al., 2004). Like Ci, GLI2 and GLI3 require PKA and an E3 ubiquitin ligase for processing to a transcriptional repressor, but GLI1 functions solely as a transcriptional activator (Hooper and Scott, 2005). Mouse mutant studies suggest that GLI2 is chiefly responsible for the activator function in response to HH signaling, and GLI3 is responsible for the repressor activity (Matisse et al., 1998; Litingtung and Chiang, 2000; Wang et al., 2000a; Pan et al., 2006). However, there are instances when GLI2 acts as a repressor (Pan et al., 2006) and GLI3 acts as an activator as seen in the developing somite (Buttitta et al., 2003). Additionally, GLI3 has been shown to act as an activator in spinal cord patterning (Bai et al., 2004). *Gli1*, but not *Gli3* is transcriptionally activated by SHH signaling which creates a positive-regulatory feedback loop (Lee et al., 1997). In mammals, GLI1 seems to have only a minor role in amplifying the transcriptional response (Park et al., 2000). It is believed that GLI2 and GLI3 are the primary transducers of HH signaling and GLI1 plays a secondary role since its expression is transcriptionally regulated by GLI2 and GLI3 (Bai et al., 2004) and *Gli1*<sup>-/-</sup> mice are viable (Park et al., 2000).

### 1.5.3 HH Signaling in Adult Neurogenesis and Tissue Homeostasis

HH acts as a long-range morphogen to control cell patterning and differentiation in several embryonic tissues (Jiang and Hui, 2008). In addition to its role in normal embryonic development, HH also plays important roles in adult tissue homeostasis. In the adult, HH continues to signal to and regulate several populations of stem and progenitor cells within various organs, including the brain (Lai et al., 2003; Machold et al., 2003; Ahn

and Joyner, 2005; Ihrie et al., 2011), skin, prostate, and bladder and others (reviewed in Petrova and Joyner, 2014). It is also required for the maintenance of stem cells in a range of tissues, from the hair follicle to the haematopoietic system, and is involved in the injury-dependent regeneration of many organs, including the exocrine pancreas, prostate, and bladder (Beachy et al., 2004; Shin et al., 2011; Lim et al., 2014).

### *Neural Stem Cells*

As mentioned in Section 1.3, in the adult mammalian brain, new neurons are generated from transit-amplifying cells (TACs) that are derived from quiescent and self-renewing neural stem cells (NSCs) located in the SVZ of the lateral ventricles and the SGZ of the hippocampal dentate gyrus (DG). *In vivo* evidence that SHH is required for the establishment of stem and progenitor cells in the SVZ and SGZ has come from conditional genetic loss-of-function studies. When HH genes or cilia are abrogated midgestation, there is a severe depletion of progenitors in the olfactory bulb and DG, suggesting that HH signaling is required for the initial establishment of NSCs (Balordi and Fishell, 2007a; Han et al., 2008). HH signaling has also been shown to be required for the continuous maintenance of neurogenesis in the SVZ and SGZ. Studies using small molecules showed that SHH gain or loss of function increases or inhibits proliferation respectively in neurogenic regions and neural stem/progenitor cells (reviewed in Petrova and Joyner, 2014). Inhibition of the pathway by removal of SMO in the majority of adult SVZ NSCs results in reduced neurogenesis (Balordi and Fishell, 2007b; Petrova et al., 2013) while over-activation of the pathway by deletion of *Ptch1* promoted NSC self-renewal at the expense of transit amplifying progenitors and neuron production (Ferent et al., 2014). This reduction in neurogenesis was linked to a shift in NSC division from

asymmetric to symmetric potentially through the induction of NOTCH signaling (Ferent et al., 2014).

### *Hair and skin*

There are multiple populations of lineage-restricted stem cells in the adult mammalian skin (reviewed in Solanas and Benitah, 2013). Like the adult brain, SHH is the main HH ligand present in postnatal skin (Petrova and Joyner, 2014). Mitotically active cells in the epithelial basal layer of the skin constantly produce new interfollicular skin cells (Petrova and Joyner, 2014). During the expansion (anagen) phase of the hair cycle, *Shh* expression is seen in the epithelial cells of the lower end of the hair follicle while the downstream effectors *Gli1* and *Ptch1* are more broadly expressed (Oro and Higgins, 2003). During the resting (telogen) phase when old hairs degenerate and die, *Gli2* and *Gli3* are broadly expressed in both the follicle and in the surrounding dermis (Petrova and Joyner, 2014), while *Gli1* and *Ptch1* expression is restricted to two distinct epithelial stem cell domains in the upper bulge and the lower bulge (Brownell et al., 2011). Inhibition of SHH with the antibody 5E1 in mice blocks the anagen progression and hair re-growth, suggesting that SHH is required for the regenerative function of adult stem cells (Wang et al., 2000b). Conversely, exogenous expression of SHH via adenoviral infection triggers the onset of the anagen phase in resting hair follicles and stimulates hair growth (Sato et al., 1999). Additionally, removal of *Shh* in the hair germ causes defects in proliferation throughout the hair follicle while genetic abrogation of *Smo* or *Gli2* alone in the stem cells reduced their proliferative abilities but did not affect anagen progression, suggesting that SHH is required to maintain the function of hair follicle stem cells but not of the progenitor cells in which it is expressed (Hsu et al., 2014).

Additionally, SHH signaling gain of function mutations are found in human basal cell carcinoma (BCC) (Hahn et al., 1996; Johnson et al., 1996; Reifenberger et al., 1998). Overexpression of *Gli1* and to a lesser extent, *Gli2* are common features of BCC (Dahmane et al., 1997; Grachtchouk et al., 2000; Oro and Higgins, 2003; Hutchin et al., 2005). SMO gain of function or PTCH1 loss of function mutations also give rise to BCC-like lesions when induced either in the mouse interfollicular epidermis or in hair follicle stem cells that move into the interfollicular skin following injury (reviewed in Petrova and Joyner, 2014), suggesting these stem cells can function as tumor-initiating cells for BCC.

### *Teeth*

Rodent incisors continue to grow throughout the life of the animal and require constant repair via stem and progenitor cells that produce ameloblasts to renew the incisor epithelium (reviewed in Petrova and Joyner, 2014). During the growth of the adult rodent incisor, SHH signals to parental *Gli1*-expressing ameloblast stem cells (Seidel et al., 2010). Inhibition of SHH signaling leads to a decrease in ameloblast production and tooth growth but does not deplete the GLI1+ stem cell population (Seidel et al., 2010), suggesting that SHH signaling is not required for stem cell survival but instead for maintaining the ability of stem cells to expand the ameloblast population. Although human teeth do not grow continuously, a multipotent stem cell population within the connective tissue surrounding the tooth was shown to express *SHH*, *GLI1*, and *PTCH1* (Martinez et al., 2011).

### *Bone*

Indian hedgehog (IHH) is one of the main regulators of chondrocyte proliferation and osteoblast differentiation during development (reviewed in Petrova and Joyner, 2014). Throughout adulthood, HH signaling continues to contribute to maintenance of the bone as administration of the SMO inhibitor, cyclopamine, to adult mice resulted in decreased bone mass and conversely, *Ptch1*<sup>+/-</sup> mutant mice exhibit a high bone mass density and *Ptch1*<sup>+/-</sup> cultured cells showed osteoblast differentiation associated with a loss of GLI3 repressor generation (Ohba et al., 2008).

### *Respiratory and gastrointestinal*

Localized upregulation of HH signaling occurs in response to an injury in the adult lung airways (Petrova and Joyner, 2014). Initially, in the normal adult mouse lung, only a few fibroblasts around the airway express *Gli1*; however, upon lung fibrosis or airway injury, HH signaling is upregulated as seen by an increase in stromal GLI1+ cells (Watkins et al., 2003; Liu et al., 2013b). Additionally, overexpression of *Shh* in the normal adult mouse airway epithelium can induce cell proliferation and lung tissue modifications similar to those seen in injury (Krause et al., 2010).

*Shh* and *Ihh* are continuously detected throughout the adult gastrointestinal tract of both humans and rodents where it signals to the *Gli*-expressing mesenchyme (reviewed in Petrova and Joyner, 2014). In the stomach of the adult mouse, HH signaling inhibits proliferation (van den Brink et al., 2001) and stimulates the differentiation (van den Brink et al., 2002) of the gastric epithelium. Additionally, the loss of IHH in the intestinal epithelium of the mouse results in a wound healing response in which there is epithelial proliferation and an ultimate loss of smooth muscle and villi (van Dop et al., 2010; Zacharias et al., 2011). When isolated mesenchyme from the intestine was treated

with SHH or IHH ligand, smooth muscle precursors decreased in number and smooth muscle cells increased in number (Zacharias et al., 2011), suggesting that HH signaling is important for smooth muscle differentiation. Overall, these studies propose that HH signaling in the intestine of the adult mouse regulates tissue homeostasis in a concentration-dependent manner.

### *Taste*

The adult fungiform taste papilla is comprised of specialized cell types that reside in a stratified squamous tongue epithelium. This sensory organ contains taste buds, papilla epithelium, and lateral walls that extend into underlying connective tissue to surround a core of lamina propria cells. The taste buds continue to differentiate and turn over postnatally throughout the life span (Beidler and Smallman, 1965; Farbman, 1980). A few studies have suggested that SHH signaling is involved in the maintenance and differentiation of taste cells. SHH ligand is produced by taste bud cells for paracrine signaling to HH-responsive cells in the basal epithelial layer, perigemmal cells, and stromal cells of the papilla and was found that these *Shh*-responding cells contribute to the maintenance of not only filiform and fungiform papillae, but also taste buds (reviewed in Liu et al., 2013a). Additionally, constitutive activation of GLI2 in the tongue epithelium led to a rapid loss of fungiform papillae and taste buds (Liu et al., 2013a), while ectopic expression of SHH induced the formation of taste buds in regions not capable of generating taste buds (Castillo et al., 2014). It was also shown that pharmacological blockade of the HH pathway with the SMO inhibitor, LDE-225, disrupted taste organs including the fungiform papillae and taste buds, and electrophysiological responses to all

taste qualities in mice (Kumari et al., 2015), suggesting that HH signaling is a principal regulator of papilla and taste bud maintenance and taste sensation.

### *Olfactory Periphery*

HH signaling in the olfactory periphery has been limited to a few studies in *Drosophila* and rats and remains largely unexplored. In *Drosophila*, HH signaling was found to play a role in OSN axon targeting that is dependent on Smo and Ihog, a co-receptor for HH ligands (Chou et al., 2010). Differential HH activity in peripheral sensory organ precursors in larva and early pupa creates OSN populations with different levels of Ptc: low-Ptc class and high Ptc class. Genetic knockdown and overexpression experiments showed that removing HH from the periphery results in loss of Ptc expression in high-Ptc OSNs which releases Smo inhibition and causes axon mistargeting similar to loss of Ptc, while brain-derived Hh is required for low-Ptc classes (Chou et al., 2010). Additionally, a recent study suggested a novel cilia-dependent role for Hh signaling in *Drosophila* that occurs in the cilia of OSNs, however, there was no evidence for the role of Hh in the OSNs (Kuzhandaivel et al., 2014). One study investigating HH signaling in the mammalian olfactory periphery found that: 1) *Shh* mRNA is expressed in mitral and tufted cells of the olfactory bulb and 2) cultured OSNs, when exposed to SHH protein, exhibit an increase in axonal branching (Gong et al., 2009), suggesting a role for HH signaling in axon branching of mammalian OSNs. This same study showed transcripts of several HH pathway components not only in the olfactory bulb, but also in the olfactory periphery, suggesting a potential role for HH signaling the adult mammalian olfactory periphery.



## 1.6 Conclusions

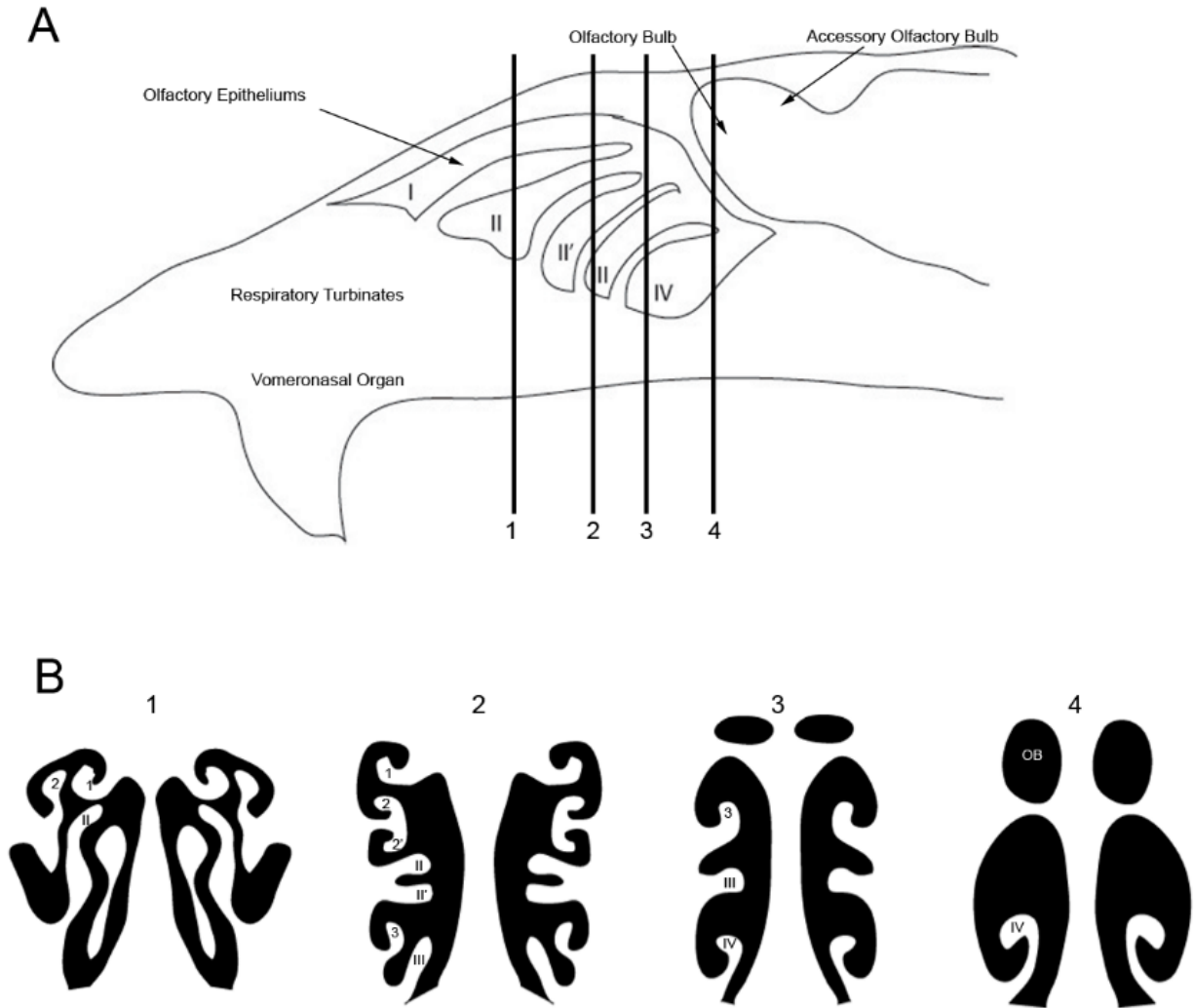
Olfaction is an important part of our everyday life and has evolved to have a large influence on our taste, memory, and behavior. Odorant detection occurs in the olfactory epithelium (OE) which is comprised of various cell types including olfactory sensory neurons (OSNs), which are necessary for the detection of smell, and the stem/progenitor cell populations, globose basal cells (GBCs) and horizontal basal cells (HBCs) (for review, see ref. Murdoch and Roskams, 2007). OSNs are unique in that they both directly contact the external environment and the brain (Doty, 2008), which exposes them and other cells in the OE to insults from toxins, bacteria, and viruses leading to cell death (Duggan and Ngai, 2007). It is known that GBCs and HBCs participate in the restoration of the OE following injury and tissue homeostasis injury (Barber, 1982; Costanzo, 1991; Iwai et al., 2008). However, olfactory dysfunction can still arise from a variety of etiologies. Treatment for more severe cases remains under investigation.

While the cell types involved in the maintenance and regeneration of the OE are known, the signaling pathways that control their activation and proliferation during normal homeostasis, and in response to injury remain largely unexplored. Various signaling factors and pathways have been investigated in the olfactory system including the involvement of Wnt and Notch signaling in the proliferation of GBCs (Cau et al., 2002; Manglapus et al., 2004; Wang et al., 2011; Krolewski et al., 2012; Chen et al., 2014). However, there has been no clear answer to which factors and pathways are directly involved in the regulation (cell division, differentiation, and fate determination) of the stem/progenitor cells, specifically HBCs. The central focus of this dissertation is to

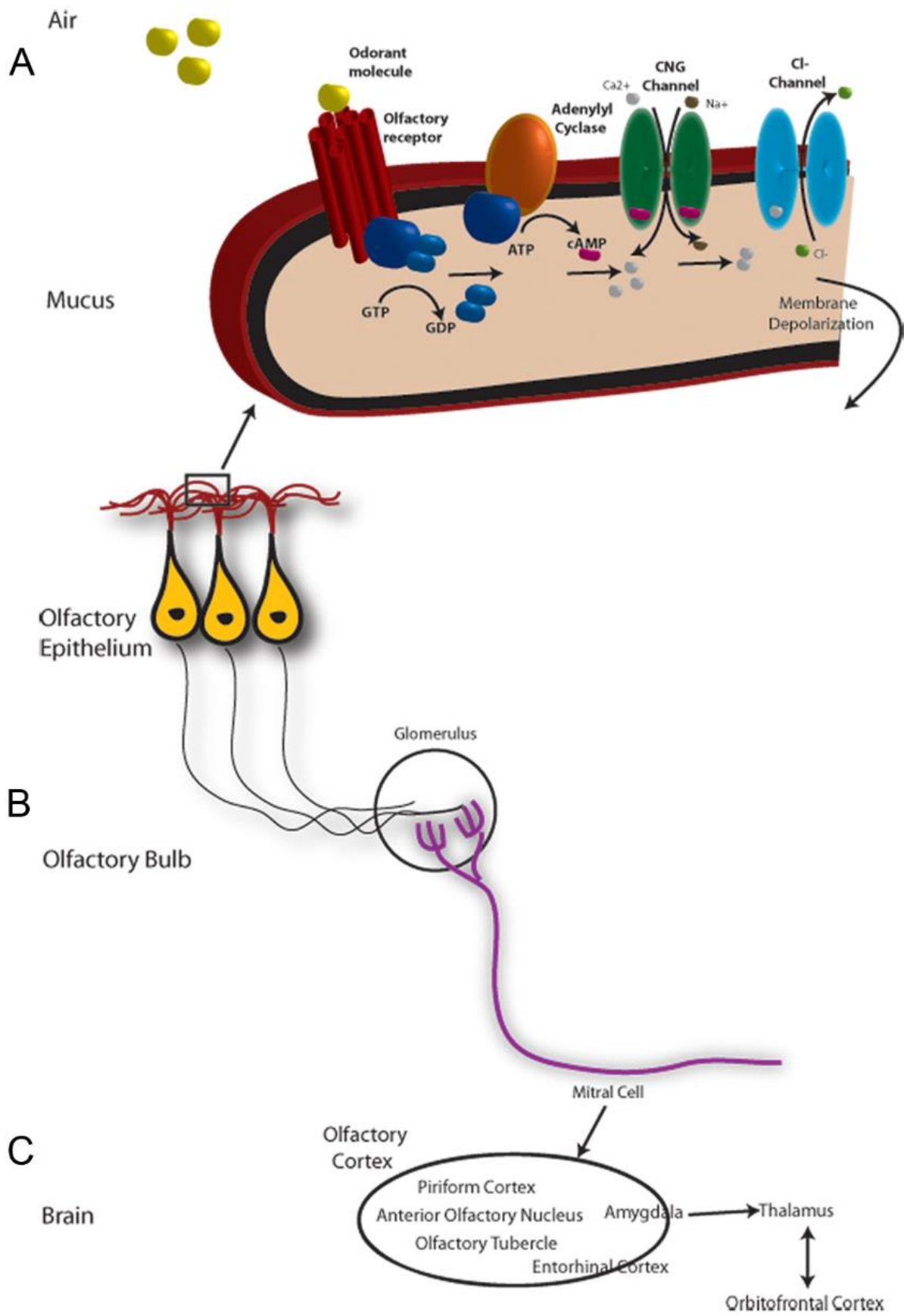
investigate specific factors involved in regulating the activity of HBCs and their contribution to neurogenesis in the OE following an injury.

Cilia have become greatly associated with stem cells in the regulation of their dormancy, proliferation, and differentiation as well as proper adult neurogenesis (reviewed in Irigoien and Badano, 2011). In Chapter II, I provide evidence of primary cilia on HBCs and indicate that OSNs are not the only ciliated cell type in the OE. I use an HBC-specific inducible system to delete cilia specifically from HBCs in order to assess the effects that a loss of HBC cilia have on OE development, homeostasis, and recovery following an injury. Disruption of cilia in systems in which cilia are important for cell proliferation and differentiation alters the activity of signaling pathways that utilize cilia, such as the HH pathway (Kumamoto et al., 2012; Tong et al., 2014). The HH pathway is not only important for the development of various tissues and organs, but also for the formation, survival, and function of stem and progenitor cell populations in several adult tissues (reviewed in Petrova and Joyner, 2014). It is an attractive candidate for regulation of HBCs due to its dependence on cilia in tissue maintenance (Croyle et al., 2011). Although HH signaling has been investigated in the SVZ and olfactory bulb (Balordi and Fishell, 2007a), and in OSN axon branching and targeting (Gong et al., 2009), it is virtually unexplored in the mammalian OE. In Chapter III, I use *lacZ* reporter mice to determine expression profiles of HH components in the OE. Additionally, I utilize an HBC-specific inducible system to target specific components of the HH pathway in order to assess the effects that HH signaling has on OE homeostasis and regeneration following an injury.

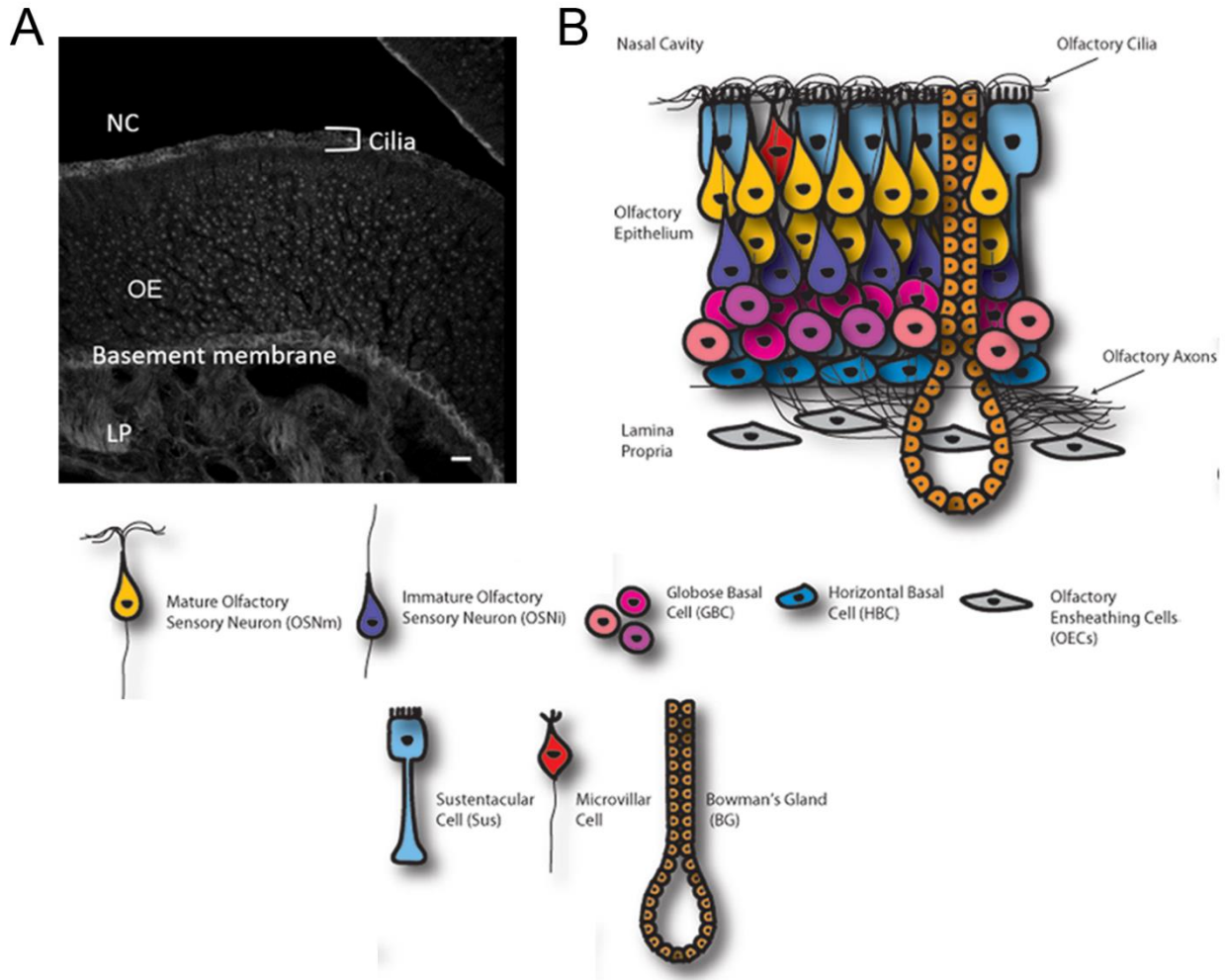
## 1.7 Figures



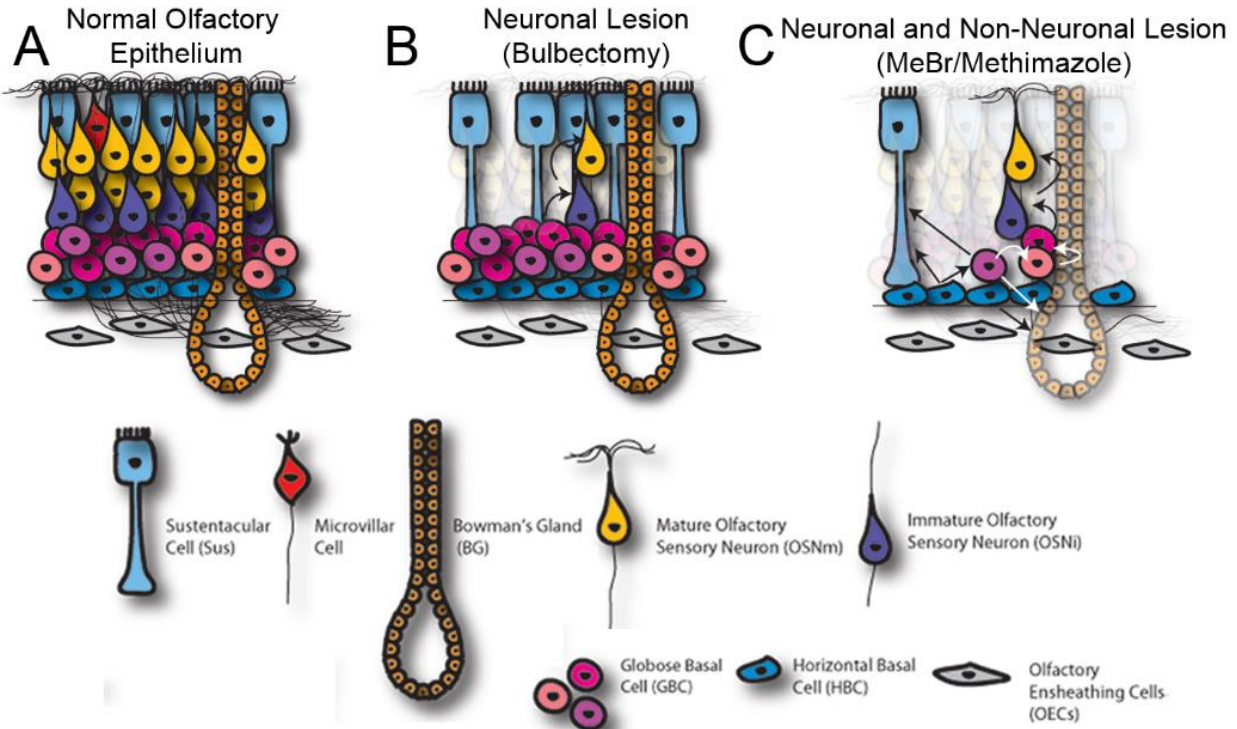
**Figure 1-1. Rodent olfactory system.** Schematic of the rodent olfactory system adapted from Adam C. Puche. **A**, Sagittal view of the mouse head depicts olfactory turbinates I-IV, olfactory bulb, and accessory olfactory bulb. **B**, Resulting coronal sections from hypothetical cuts 1-4. Roman numerals represent endoturbinates and numbers represent ectoturbinates.



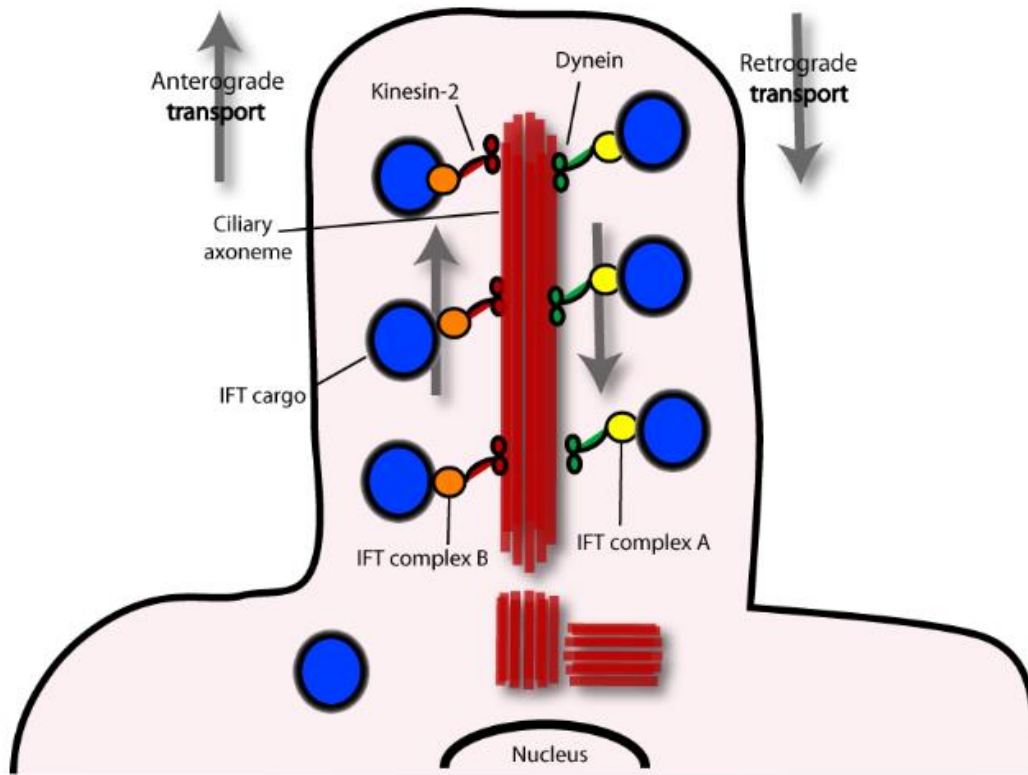
**Figure 1-2. Olfactory transduction pathway.** Schematic of the olfactory transduction pathway. **A**, All olfactory signaling machinery is found in the cilia of olfactory sensory neurons (OSNs). Upon an odorant binding to its corresponding olfactory receptor (OR), the G-protein,  $G\alpha_{olf}$ , is activated resulting in the activation of adenylyl cyclase II (ACII) and production of cyclic AMP (cAMP). This increase in cAMP opens cyclic nucleotide-gated (CNG) channels leading to an influx of sodium ( $Na^+$ ) and calcium ( $Ca^{2+}$ ) ions and depolarization of OSNs. This depolarization is further amplified by activation of calcium-activated chloride ( $Cl^-$ ) channels. **B**, OSNs project axons to corresponding structures in the olfactory bulb (OB) known as glomeruli, where they form synapses with dendrites of mitral and tufted cells. **C**, These projection neurons extend their axons to the olfactory cortex which is comprised of several areas including the piriform cortex, olfactory tubercle, anterior olfactory nucleus, and specific parts of the amygdala and entorhinal cortex.



**Figure 1-3. Cell composition of the olfactory epithelium.** **A**, Immunofluorescent image of the mouse OE in grayscale showing the cilia layer of the OE within the nasal cavity and the separation of the OE from the lamina propria (LP) by the basement membrane. **B**, Schematic illustration depicting the various cell types in the OE and LP. Microvillar and SUS cells project microvilli into the nasal cavity, while mature OSNs project cilia. Immature OSNs do not possess cilia but like mature OSN, extend axons into the LP that traverse to the olfactory bulb. Globose basal cells are comprised of a heterogeneous population of cells that can be grouped into two main types of cells due to their expression of distinct transcription factors: immediate neuronal progenitors, transit-amplifying precursors committed to producing neurons, and multi-potent precursors that can produce non-neuronal cells. They lie just below immature OSNs and above horizontal basal cells which lie just against the basement membrane. Olfactory ensheathing cells are found in the lamina propria. NC = nasal cavity, OE = olfactory epithelium, and LP = lamina propria.

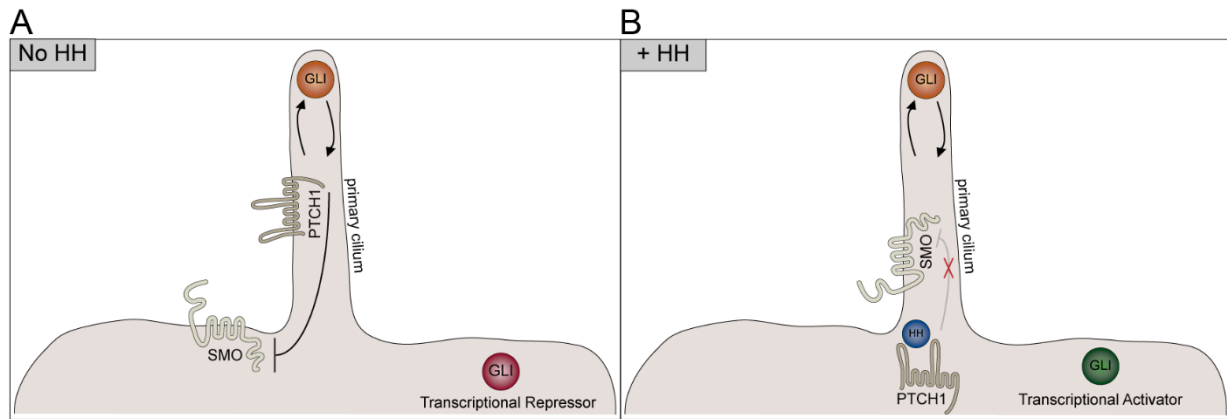


**Figure 1-4. Differentiation pathways of olfactory basal stem cells.** Schematic illustration depicting various cell types of the OE and the differentiation pathways of basal stem cells at varying levels of injury to the OE. **A**, Cell types of the normal, unlesioned OE. **B**, During a neuronal-specific lesion, as seen with olfactory bulbectomy models, GBCs are the lead contributor to replacing OSNs through differentiation. **C**, However, in more severe lesion models such as ablation with MeBr or the anti-thyroid drug, methimazole (MMI), in which SUS cells, BG cells, and GBCs are also depleted, HBCs replenish neuronal cells (neuronal precursor GBCs) and non-neuronal cells (multipotent GBCs, SUS cells, and BG cells) of the OE through differentiation. GBCs are believed to differentiate into non-neuronal cells (SUS cells and BG cells) from a sub-population of multipotent cells and neuronal cells (neuronal precursor GBCs and OSNs) from a sub-population of transit-amplifying GBCs. OE = olfactory epithelium.

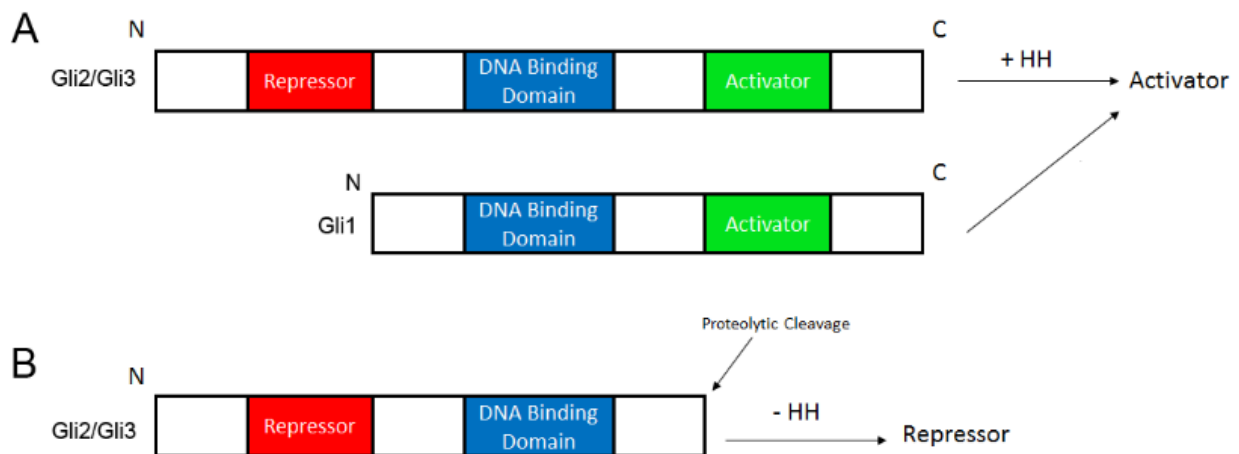


**Figure 1-5. Cilia machinery and trafficking.** Schematic illustration showing the cilium and its trafficking components adapted from (Hildebrandt et al., 2011). Centrioles form basal bodies, comprised of 9 sets of microtubules, from which the axoneme extends. Intraflagellar transport (IFT) proteins mediate the assembly and maintenance of the cilium by associating with kinesin motors to bring cargo into the cilium for anterograde transport and associating with dynein motors to bring cargo out of the cilium for retrograde transport. Kinesin motors associate with 2 distinct complexes of IFT proteins: complex A for anterograde trafficking and complex B for retrograde trafficking.





**Figure 1-6. Canonical Hedgehog pathway.** Schematic illustration depicting the canonical Hedgehog (HH) pathway in mammals. **A**, In the absence of HH ligand, the transmembrane receptor Patched1 (PTCH1), inhibits the transmembrane protein Smoothed (SMO), resulting in the transcriptional repression of HH target genes by GLI transcription factor. **B**, In the presence of HH ligands, which bind to PTCH1, de-repressed SMO, which traffics into cilia, allows for the activation of GLI transcription factors and HH target genes.



**Figure 1-7. GLI processing in the Hedgehog pathway.** Schematic illustration showing the processing of GLIs into activators and repressors. **A**, All GLI proteins have a DNA-binding domain and C-terminal activation domain while GLI1 has diverged evolutionarily to lack a transcriptional repressor domain. In the presence of HH ligand, activation of SMO inhibits the proteolytic processing of GLI2 or in certain circumstances, GLI3, allowing the full length protein to act as a transcriptional activator. **B**, In the absence of HH ligand, GLI3 and to a lesser degree, GLI2, are processed as a transcriptional repressor upon proteolytic cleavage of the C-terminal activation domain. N = N-terminus, C = C-terminus, and HH = hedgehog.

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## CHAPTER II:

# Primary Cilia on Horizontal Basal Cells Regulate Regeneration of the Olfactory Epithelium

### 2.1 Abstract

The olfactory epithelium (OE) is one of the few tissues to undergo constitutive neurogenesis throughout the mammalian lifespan. It is comprised of multiple cell types including olfactory sensory neurons (OSNs) that are readily replaced by two populations of basal stem cells, frequently dividing globose basal cells (GBCs) and quiescent horizontal basal cells (HBCs). However, the precise mechanisms by which these cells mediate OE regeneration are unclear. Here, we show for the first time that the HBC subpopulation of basal stem cells uniquely possess primary cilia that are aligned in an apical orientation in direct apposition to sustentacular cell endfeet. The positioning of these cilia suggests that they function in the detection of growth signals and/or differentiation cues. To test this idea, we generated an inducible, cell-type specific *Ift88* knockout mouse line (*K5rtTA;tetOCre;Ift88<sup>fl/fl</sup>*) to disrupt cilia formation and maintenance specifically in HBCs. Surprisingly, the loss of HBC cilia did not affect the maintenance of the adult OE but dramatically impaired the regeneration of OSNs following lesion. Furthermore, the loss of cilia during development resulted in a region-specific decrease in neurogenesis, implicating HBCs in the establishment of the OE. Together, these

results suggest a novel role for primary cilia in HBC activation, proliferation, and differentiation.

## **2.2 Introduction**

Neurogenesis occurs from the self-renewal and differentiation of neural stem cells (Gage, 2000). While prevalent during development, neural stem cells are also found in the adult nervous system, in the olfactory epithelium (OE), subventricular zone (SVZ) of the lateral ventricle, and the subgranular zone (SGZ) of the hippocampus (Gage, 2000; Alvarez-Buylla and Garcia-Verdugo, 2002; Lie et al., 2004). Factors and mechanisms that regulate proliferation, migration, differentiation, and cell survival during development can be active in the adult nervous system, allowing for tissue repair and neuroplasticity (reviewed by Lie et al., 2004). Unlike most sensory systems, the OE is able to reconstitute both neuronal and non-neuronal populations following injury and neuronal death via the action of resident populations of olfactory stem cells (Graziadei and Graziadei, 1979; Calof and Chikaraishi, 1989; Edge and Chen, 2008). Olfactory sensory neurons (OSNs) are unique in that they both directly contact the external environment and the brain. While this direct contact allows OSNs to detect odors, it also exposes the OE to insults from toxins, bacteria, and viruses leading to cell death. Therefore, the capacity for neurogenesis and replacement of OSNs is critical for maintaining this important sensory system.

The OE is composed of OSNs, supporting sustentacular (SUS) cells, Bowman's gland (BG) duct cells, and two groups of basally located stem cells, globose basal cells

(GBCs), and horizontal basal cells (HBCs). GBCs and HBCs are considered progenitor or stem cells of the OE, capable of promoting regeneration and neurogenesis both for tissue homeostasis and in response to injury (Barber, 1982; Costanzo, 1991; Leung et al., 2007). GBCs are a heterogeneous population of actively cycling cells comprised of immediate neuronal progenitors and transit-amplifying precursors committed to producing neurons as well as multi-potent precursors that can produce non-neuronal cells (Jang et al., 2014). HBCs are a homogeneous population of multi-potent, quiescent cells (Holbrook et al., 1995; Carter et al., 2004; Iwai et al., 2008). Following the selective death of olfactory neurons, as occurs in response to an olfactory bulbectomy, GBCs replace OSNs through differentiation, while HBCs remain quiescent (Caggiano et al., 1994; Huard et al., 1998; Leung et al., 2007). In severe lesion models such as exposure to methyl bromide or ablation with methimazole (MMI), in which SUS cells and GBCs are affected, HBCs contribute to the regeneration of the OE (Leung et al., 2007; Iwai et al., 2008). While the cell types involved are known, the precise mechanisms controlling regeneration and homeostasis are unclear. Importantly, the molecular regulation of olfactory basal stem cells, including their activation and proliferation in response to injury and cell fate determination during differentiation, remains largely unknown.

Primary cilia have important roles in cell proliferation, differentiation, and regulation of the cell cycle (reviewed by Irigoien and Badano, 2011). There is growing evidence that primary cilia regulate neurogenesis and/or proper differentiation of adult stem cells into amplifying progenitor cells or glial cells in the SVZ and hippocampus (Amador-Arjona et al., 2011; Kumamoto et al., 2012; Tong et al., 2014). Consequently, when cilia are disrupted in these systems, cilia-dependent signaling pathways such as Wnt and SHH



are also disrupted (Kumamoto et al., 2012; Tong et al., 2014). These findings demonstrate the important role cilia play in signaling pathways essential for proper cell differentiation during development and adult homeostasis.

Here, we show that HBCs possess primary cilia, suggesting a potential mechanism for the molecular regulation of olfactory basal stem cells in the OE. In mice with a HBC-specific cilia deletion, the OE showed limited regeneration following lesion, with a significant reduction of mature OSNs. Additionally, when HBC cilia were removed early in development, specific regions of the OE were found to have a significant reduction in OSNs. These data identify HBC cilia as a previously unrecognized signaling structure in the OE, provide mechanistic insight into the regulation of HBCs during olfactory regeneration, and indicate a potential role for HBCs in OE development.

## **2.3 Results**

### *Olfactory stem cells possess primary cilia.*

ARL13B is a small Ras GTPase that regulates ciliogenesis and cilia function (Cantagrel et al., 2008; Higginbotham et al., 2013; Kasahara et al., 2014; Bangs et al., 2015). While immunostaining the OE of wild-type mice for endogenous ARL13B, we made a fortuitous discovery of what appeared to be cilia projecting from cells located just above the lamina propria (Fig. 2-1). To determine if these primary cilia were on a specific olfactory cell type we immunolabeled the OE for the basal body marker gamma ( $\gamma$ ) tubulin and the nuclear transcription factor p63, which labels HBCs (Packard et al., 2011). The staining revealed ARL13B+ cilia projecting from basal bodies located within HBCs (Fig.

2-1A-B). To confirm the presence of cilia using a transgenic marker, we analyzed the OE of mice expressing an ARL13B-GFP fusion protein (*Ar13b-EGFP<sup>tg</sup>*) (Delling et al., 2013) labeled with a second HBC marker, Keratin5 (K5) (Holbrook et al., 1995). Similar to the endogenous staining, ARL13B:GFP also labels cilia structures projecting from HBCs (Fig. 2-1C). To further characterize HBC cilia, we stained the OE for additional ciliary markers. Adenylyl cyclase III (AC3) is a canonical marker of cilia projecting from OSNs, but also labels cilia present on other cell types including primary neurons and astrocytes (Bishop et al., 2007; Guadiana et al., 2013; Higginbotham et al., 2013). AC3 co-localizes with endogenous ARL13B (Fig. 2-1D) in wildtype mice, as well as ARL13B:GFP (Fig. 2-1E) in transgenic mice. The AC3+ cilia are also associated with p63 labeled HBCs similar to ARL13B (Fig. 2-1F). Finally, we used a second transgenic mouse, *EGFP-Cetn2*, as an additional label for basal bodies (Higginbotham et al., 2004; Bangs et al., 2015). Staining tissue with AC3 antibodies revealed AC3+ projections associated with EGFP-CETN2 labeled basal bodies (Fig. 2-1G). Together, these data suggest that HBCs possess primary cilia and indicate that OSNs are not the only ciliated cell type in the OE.

In the OE, apically located SUS cells possess basal projections, known as endfeet, that juxtapose olfactory basal cells en route to contact with the basal lamina (Doyle et al., 2001). The purpose of these connections has yet to be elucidated; however, it has been proposed that this is a site for communication between basal cells and SUS cells (Jia and Hegg, 2010). In our analysis, we observed that the majority of HBC cilia project from the top of the HBCs towards the SUS cell endfeet. To determine if HBC cilia are associated with SUS cell endfeet, analysis of p63+ HBCs and SUS cells immunolabeled with Keratin18 (K18) (Holbrook et al., 2011) was carried out in *Ar13b-EGFP<sup>tg</sup>* mice. As seen

in a representative image, cilia projecting from HBCs are in apposition to the endfeet (Fig. 2-1H). To improve the resolution of a single SUS cell endfoot, we analyzed the OE of mice intranasally injected with an adenovirus expressing GFP, in which a small subset of SUS cells are transduced (for methods, see ref. McIntyre et al., 2012). Using this approach, we observed that the ARL13B+ cilium projects into the interstitial space between the HBC and SUS cell (Fig. 2-1I). These data suggest the potential for cilia to act as an antenna for communication between basal cells and SUS cells perhaps in a manner analogous to the immunological synapse (Bromley et al., 2001; Finetti et al., 2011).

*Cilia are present on distinct subpopulations of olfactory stem cells.*

Given the close proximity of GBCs and HBCs at the base of the OE, we assessed whether GBCs also possess primary cilia. We identified a novel pan-GBC marker to distinguish between HBC and GBC subpopulations. SEC8 is one of eight subunits in the exocyst complex that was initially discovered in the secretory pathway of yeast *S. cerevisiae* and proposed to contribute to various mechanisms, including protein synthesis and vesicle trafficking (Wang et al., 2004). Antibody staining for SEC8 in the OE specifically labels a large population of GBCs overlapping with previous identified markers of GBC subpopulations (Fig. 2-2A). Immunostaining with antibodies to either MASH1 (also known as ASCL1) (Manglapus et al., 2004), a basic helix-loop-helix transcription factor that is required in the early stages of olfactory neuron lineage (Cau et al., 1997) or, LSD1 (lysine-specific demethylase 1), a chromatin modifying complex protein (Krolewski et al., 2013) in conjunction with SEC8 confirmed that SEC8 is indeed a pan-GBC marker. All MASH1+ or LSD1+ cells appear to co-express SEC8 (Fig. 2-2A). Approximately 41%

of SEC8+ cells were MASH1+, while approximately 90% of SEC8+ cells were also LSD1+ (Fig. 2-2A, C; N=4). Labeling of the OE with ARL13B and SEC8 antibodies revealed that very few (<5%) SEC8+ GBCs possess cilia, while >70% of K5+ HBCs possess cilia (Fig. 2-2B, D; N=6). These data show that HBCs are the predominant ciliated olfactory basal stem cells and suggest a specific role for cilia in this subpopulation of neural progenitors.

*Conditional deletion of IFT machinery results in the specific loss of cilia on HBCs.*

To study the cell autonomous function of cilia in HBCs, we used a floxed allele for a gene essential for intraflagellar transport (*Ift88*) and an inducible Cre driver specific to HBCs in the OE (see methods). IFT88 is a critical component of the bi-directional intraflagellar transport (IFT) system (Singla and Reiter, 2006; Pedersen and Rosenbaum, 2008) and conditional knockout of *Ift88* ablates cilia from specific cell types (Croyle et al., 2011; Sharma et al., 2013). Mice in which HBC cilia were ablated (*K5rtTA;TetOCre;Ift88<sup>fl/fl</sup>* and *K5rtTA;TetOCre;Ift88<sup>fl/Δ</sup>*) are hereafter referred to as iHBC-IFT88 mice, while phenotypically wildtype mice (*K5rtTA;TetOCre;Ift88<sup>fl/wt</sup>*) are hereafter referred to as control mice.

Control and iHBC-IFT88 mice were administered a doxycycline-containing (dox) diet to activate Cre expression (Gunther et al., 2002; Grachtchouk et al., 2011) at postnatal day 28 (P28), when the OE is mature (Murdoch and Roskams, 2007). One week post dox administration, ~90% of HBCs in mice with both *TetO-Cre* and *K5rtTA* alleles show Cre expression (Fig. 2-3A). Cre expression was not detected in HBCs of mice that lacked the *TetOCre* allele (Fig. 2-3B). More importantly, iHBC-IFT88 mice show a significant loss (88.5%) of ciliated HBCs after 4 weeks of dox (Fig. 2-3C-D, N=5). Interestingly, loss of cilia does not result in a change in the number of HBCs (Fig. 2-3E,

N=5). Immunostaining with the mature OSN marker, olfactory marker protein (OMP), and acetylated  $\alpha$ -tubulin (Acet-Tub) revealed no changes in OSN composition (Fig. 2-3F). An increase in cilia loss on HBCs (95.6%) was detected after 8 weeks of dox administration (Fig. 2-4A-B), with no effect on the number of HBCs (Fig. 2-4C), GBCs (Fig. 2-4D-E) and OSNs (Fig. 2-4F-G) (Control mice N=2, iHBCIFT88 mice N=4). These data demonstrate that genetic ablation of *Ift88* efficiently removes cilia from HBCs, without altering HBC quiescence or the normal maintenance of the OE.

*Loss of cilia in HBCs results in improper regeneration of the olfactory epithelium following injury.*

HBCs are believed to be a quiescent population of cells unless activated by severe injury to participate in OE regeneration (Leung et al., 2007). Methimazole (MMI) is an olfactory toxicant whose metabolites induce cell death of OSNs, SUS cells, and GBCs but spares HBCs in the mouse OE (Brittebo, 1995; Packard et al., 2011). Four weeks after dox administration, iHBC-IFT88 and control mice were given an intraperitoneal injection of MMI (75 mg/kg) to chemically lesion the OE, and analyzed at 8 weeks post-recovery (Genter et al., 1995; Bergman and Brittebo, 1999). The presence of cilia on HBCs remained significantly reduced in iHBC-IFT88 mice after recovery (Fig. 2-5A, C; N=5 for both groups), while no difference in the number of HBCs was observed between iHBC-IFT88 and control mice, as indicated by the number of K5+ cells (Fig. 2-5A, D; N=5 for both groups). Surprisingly, there was a significant reduction in the number of SEC8+ GBCs in iHBC-IFT88 mice compared to controls (Fig. 2-5B, E; N=5 for both groups). In addition, the number of OMP+ mature OSNs was reduced by approximately 75% in iHBC-IFT88 mice (Fig. 2-5F, G; N=5 for both groups). Consequently, the thickness of the OE

was also reduced by approximately 50% (Fig. 2-5H; N=5 for both groups). Interestingly, no change in the number of cleaved caspase-3+ cells was observed between control and iHBC-IFT88 mice 8 weeks post-recovery, suggesting that the reduction of mature OSNs and thickness of the OE was not due to increased cell death (Fig. 2-5I, J; N=5 for both groups).

While the regeneration of neurons was not completely eliminated, the OSNs that returned possess acetylated  $\alpha$ -tubulin labeled cilia (Fig. 2-5F). Since IFT88 is required for OSN cilia (McIntyre et al., 2012), the presence of ciliated OSNs in the regenerated OE suggests that these OSNs were derived from progenitors other than HBCs lacking IFT88. In our iHBC-IFT88 mice that were administered dox for 4 weeks, approximately 12% of HBCs still possessed cilia (see results above). Based on our MMI lesion paradigm, it is therefore possible that this remaining 12% of ciliated HBCs, in which IFT88 is present, contributed to regeneration of the OE. However, another possible explanation is that these OSNs were derived from residual GBCs and not from HBCs lacking IFT88. This notion is consistent with MMI lesion, which can leave residual GBCs (Xie et al., 2013). Nonetheless, such significant reduction of OSNs should coincide with a decline in synaptic input into the olfactory bulb (OB), which can be measured by the expression of tyrosine hydroxylase (TH) in the dopaminergic interneurons of the OB (Baker et al., 1993; Baker et al., 1999). Following recovery there was a significant reduction in the intensity of TH in the bulb of iHBC-IFT88 mice compared to control mice (Fig. 2-5K-L; N=4 for both groups) and the glomerular perimeter was significantly reduced. Together, these data indicate that without cilia, HBCs are unable to contribute to the regeneration of the OE,

potentially due to disrupted HBC proliferation, resulting in impaired OSN recovery and olfactory function.

In order to link the observed effects to cilia function, and not off-target effects of IFT88 loss (Robert et al., 2007), we repeated these experiments using a cell-specific knockout of *Arl13b* (Caspary et al., 2007; Larkins et al., 2011). ARL13B is specifically localized to the cilia membrane and is required for proper ciliogenesis (Caspary et al., 2007). Moreover, mutations in *Arl13b*, lead to loss of cilia phenotypes as well as HH-related phenotypes due to the disruption in the localization and ciliary targeting of HH pathway components (Caspary et al., 2007; Duldulao et al., 2009; Larkins et al., 2011). *K5rtTA;TetOCre;Arl13b<sup>fl/fl</sup>* mice (referred to hereafter as iHBC-ARL13B mice) and *K5rtTA;TetOCre;Arl13b<sup>fl/wt</sup>* mice (referred to hereafter as control mice) underwent the same MMI lesion paradigm as stated above. After 8 weeks of recovery, ARL13B+ HBC cilia were observed in control mice but not in iHBC-ARL13B mice (Fig. 2-6A). Similar to results observed in iHBC-IFT88 mice, the number of HBCs did not differ between control and iHBC-ARL13B mice (Fig. 2-6B; N=3 for both groups). Additionally, there was a significant reduction (~ 30%) in the number of SEC8+ GBCs (Fig. 2-6C-D; N=3 for both groups) as well an approximate 75% reduction in the number of OMP+ mature OSNs (Fig. 2-6E-F; N=3 for both groups) in iHBC-ARL13B mice compared to controls. Interestingly, the apical surface of the OE of iHBC-ARL13B mice had reduced Acet-Tub labeled OSN cilia. Together, these results not only recapitulate those observed in the iHBC-IFT88 mice but also suggest that *Arl13b* is required for HBC cilia function and regeneration of the OE.

*Depletion of HBC cilia results in the impaired development of the OE.*

In mice, the OE begins to form at embryonic day 10 (E10) (Murdoch and Roskams, 2007). Small numbers of p63-expressing cells first appear at E14, after the emergence of all other cell types (Packard et al., 2011). Therefore, HBCs are not believed to participate in the establishment of the OE. HBCs settle to the basal lamina, begin to express K5, and become dormant between ~E16 and P10 (Packard et al., 2011). In order to exploit this late development, iHBC-IFT88 mice were administered dox starting at E16 for 4.5-5 weeks to ablate cilia during OE maturation. At P28, iHBC-IFT88 mice had a near complete loss of cilia on HBCs across all regions of the OE compared to control mice (Fig. 2-7A-B; N=5 for both groups), with no difference in the total number of HBCs (Fig. 2-7A, C; N=5 for both groups). Interestingly, the dorsal lateral region associated with ectoturbinate 2 and 2', exhibited a significantly reduced number of OMP+ mature OSNs in iHBC-IFT88 mice (Fig. 2-8A-H). While other regions of the OE also exhibit a reduction in the number of mature OSNs, this reduction was variable along the anterior-posterior axis of the OE and most pronounced near the midpoint of the anterior-posterior axis. Quantitation of OMP+ neurons in the posterior OE revealed a reduction in mature OSNs in the dorsal medial and dorsal lateral regions but not the ventral medial and ventral lateral OE (Fig. 2-8E, I; N=5 for both groups). These data show that cilia on HBCs are important for proper neurogenesis during development of the OE, providing evidence that HBCs participate in the establishment of this tissue that was thought to be limited to GBCs (Treloar et al., 2010).



## 2.4 Discussion

Within the olfactory system, it is well known that cilia from individual OSNs create a large receptive field in which an OSN can be activated by an odorant (for review, see DeMaria and Ngai, 2010). Until now it was widely believed that neurons were the sole ciliated cell type in the OE. Here, we show for the first time that primary cilia exist on a reserve population of olfactory basal stem cells, the HBCs. Furthermore, utilizing the genetic deletion of two cilia-specific genes in HBCs, we demonstrate that primary cilia are critical for activation of the regenerative capacity of HBCs following chemical lesion. While *Ift88* plays a critical role in ciliogenesis and maintenance, it has also been implicated in G1-S transition in ciliated cells (Robert et al., 2007). However in other studies targeted deletion of *Kif3a*, a kinesin motor important for cilia function, shows similar phenotypic effects observed with loss of *Ift88* suggesting a common mechanism of action through the cilium (Berbari et al., 2009; Wong et al., 2009). In our study we have validated the results observed with deletion of *Ift88* by the targeted removal of *Arl13b*. The loss of *Arl13b* has previously been demonstrated to affect neural development, and mutations in *Arl13b* underlie human ciliopathies (Caspary et al., 2007; Cantagrel et al., 2008; Higginbotham et al., 2012; Zhang et al., 2013). As IFT88 and ARL13B serve different roles in cilia function, the similar phenotypes observed in two different mutant lines supports the conclusion that the loss in regenerative capacity of HBCs is due to dysfunctional primary cilia.

HBCs are long-lived quiescent progenitors that are activated only after extensive lesion of the OE in which SUS cells and GBCs are depleted (Leung et al., 2007). The mechanism by which HBCs become activated remains unknown; however, SUS cell

endfeet have been previously shown to terminate on HBCs (Holbrook et al., 1995). Given that the present findings demonstrate an anatomical localization of the HBC cilia relative to SUS cell endfeet, we propose a model in which HBC cilia act to sense cues from the SUS cells regarding the health of the OE. We propose that this communication occurs at the interface between SUS cell endfeet and HBC cilia (Fig. 2-9A). This paradigm may be analogous to the immunological synapse that forms between a T cell and an antigen-presenting cell functioning to orchestrate signals that drive T cell activation (for review, see Bromley et al., 2001). Following injury to the OE, signaling is conceivably altered between SUS cells and HBCs resulting in activation of the quiescent HBCs (Fig. 2-9B). Without cilia, HBCs are unlikely to detect signals necessary for proliferation and/or differentiation (Fig. 2-9C). Additional support for a SUS/HBC connection in regenerating the OE comes from different lesion models. In OSN-specific lesions, where SUS and GBC cell death is spared, HBCs remain quiescent, and the GBCs are the leading contributor to regeneration (Leung et al., 2007; Makino et al., 2009). However, when lesions result in SUS and GBC cell death, HBCs become active and contribute to regeneration (Leung et al., 2007; Jia et al., 2010). These findings suggest that death of SUS cells stimulates HBCs to proliferate and contribute to regeneration. However, an alternative explanation that cannot be ruled out based on current lesion models is whether signaling occurs between GBCs and HBCs, and how such signaling may contribute to HBC proliferation and OE regeneration. Interestingly, negative feedback signaling is known to occur in the OE, as is observed between neuronal and stem/progenitor cells, in order to control self-replication and differentiation of the stem progenitor cell population (Beites et al., 2005; Gokoffski et al., 2010). It is therefore plausible that such feedback signaling may occur

between GBCs and HBCs via HBC cilia, and that this signaling is lost when lesion results in GBC cell death. In either case, whether the injury results in the release of a stimulatory signal, or the loss of a tonic inhibitory cue between HBCs and other cell types remains to be determined.

Quiescent adult stem cells typically forgo cell cycle decisions in order to respond to transient environment signals sensed through the cilia (Plotnikova et al., 2009). These signals include the Notch, Wnt, and HH pathways, each of which is strongly linked to neurogenesis in the brain (Kumamoto et al., 2012; Tong et al., 2014). The Wnt pathway has been previously implicated in OE proliferation and neurogenesis during development and regeneration (Wang et al., 2011; Chen et al., 2014). In contrast, Notch signaling appears to participate in development of supporting cells but not neurons in the OE (Manglapus et al., 2004; Krolewski et al., 2012). Currently, there is no evidence for the role of the HH pathway in OE development. However, canonical HH signaling is strongly linked to cilia in numerous other systems (for review, see Goetz and Anderson, 2010). Numerous HH pathway components dynamically localize to cilia, while disruption of cilia results in aberrant HH signal transduction and impaired morphogenesis in specific organ systems (for review, see Berbari et al., 2009).

While the signaling pathways may be shared, the phenotypic effects of cilia loss differ between ciliated cell types including various stem cells. In the adult skin, loss of cilia on basal cells resulted in the proliferation of cells in the interfollicular epidermis with subsequent perturbation of epidermal homeostasis (Croyle et al., 2011). In contrast, the conditional ablation of primary cilia postnatally from neural stem cells (NSCs) in the hippocampus led to a reduction in amplifying progenitor cells without altering the number

of quiescent NSCs (Amador-Arjona et al., 2011). In addition, primary cilia in the cerebellum are required for expansion of the neural progenitor pool (Chizhikov et al., 2007). Similarly, a recent report suggested that localized ablation of cilia in NSCs in the ventricular–subventricular zone (V-SVZ) decreases neurogenesis only in the ventral V-SVZ (Tong et al., 2014). These data in NSCs are similar to what we observed with a loss of cilia from HBCs in the OE– no change in the number of HBCs, but a reduction in the neurogenesis of the OE. Together, these data suggest the convergence of a common cilia ablation phenotype between neural stem cells as opposed to epidermis.

During development, NSCs are important for early neurogenesis and morphogenesis of the OE (Gokoffski et al., 2010). While maturing GBCs that migrate from the apical surface clearly contribute to organogenesis (Cau et al., 2002), the precise role of HBCs is unclear. Evidence from a lineage-trace mouse model suggests that upon their establishment in the OE at P10, HBCs do participate in neurogenesis (Iwai et al., 2008). Our data supports the notion of HBC-driven neurogenesis in early postnatal development of the OE and suggests that cilia on HBCs are required for normal OE development. Interestingly, the loss of OSNs observed in the developing OE was regional whereas in the recovering OE it was global. We speculate that these differences can be attributed to the temporal and spatial release of morphogens during development that are synchronized after severe injury to the OE (Vedin et al., 2009). Nevertheless, our data demonstrate a clear role for HBCs and their cilia in the developing OE.

Our finding of cilia on HBCs and their importance in neurogenesis reveals a potential novel mechanism for the etiology of olfactory dysfunction. It is now well recognized that anosmia is a clinical manifestation of ciliopathies, a growing class of

pleiotropic genetic disorders, traditionally associated with the loss of cilia on OSNs. However, the ability to maintain a functional olfactory system throughout life depends on the presence of a stem cell population. While the OE undergoes constant neurogenesis, there is a net loss of neurons over time due to reduced stem cell function (Ducray et al., 2002; Conley et al., 2003). Changes that alter cilia function on HBCs could hasten this decline and contribute to age related olfactory loss. Moreover, ciliopathy patients may show increased susceptibility to chemical insult to the OE. Work here suggests that impaired neurogenesis may be a new unforeseen mechanism for olfactory dysfunction in congenital anosmias.

## 2.5 Materials and Methods

*Mouse strains and Genotyping.* All mice were maintained on a mixed genetic background. Transgenic *Arl13b-EGFP<sup>tg</sup>* mice were provided by David Clapham (Harvard University). *EGFP-Cetn2* mice were obtained from The Jackson laboratory (stock number 008234) (Higginbotham et al., 2004). Conditional deletion of *Ift88* from olfactory HBCs was achieved by the use of a doxycycline-inducible Cre mouse model. This model utilized mice carrying three alleles: (a) a K5-promoter driving expression of the reverse tetracycline transactivator (rtTA) (*K5rtTA*) (Diamond et al., 2000), (b) a tetracycline Operator (TetO) to permit expression of Cre (*TetOCre*) (Mucenski et al., 2003), and (c) a floxed *Ift88<sup>fl/Δ</sup>* to ablate cilia (the  $\Delta$  allele has exons 4-6 deleted from *Ift88*) (Haycraft et al., 2007). *K5rtTA* and *TetOCre* mice were provided by Dr. Andrzej Dlugosz (University of Michigan, Ann Arbor, MI). *Ift88<sup>fl/Δ</sup>* mice were provided by Dr. Bradley Yoder (University of Alabama at Birmingham, Birmingham, AL). Removal of *Arl13b* from olfactory horizontal

basal cells was achieved using a similar strategy with a floxed *Arl13b* (exon 2) mouse provided by Dr. Tamara Caspary (Emory University). All mice of either sex were housed and maintained according to the University of Michigan and University of Florida institutional guidelines. All protocols for mouse experimentation were approved by the University of Michigan and the University of Florida Committee(s) on the Use and Care of Animals. Genotyping was performed using primers and PCR parameters from previously published work referenced above.

*Doxycycline Transgene Induction and olfactory epithelium lesion.* Mice were fed doxycycline chow (200 mg/kg doxycycline, Bio-Serv) and water (200µg/ml doxycycline, 5% sucrose, Fisher) starting at either embryonic day 16 (E16) or postnatal day 28 (P28) and remained on doxycycline diet until the time of euthanasia. Based on an approximate daily food intake of 4 g/mouse and water intake of 6ml/mouse (Bachmanov et al., 2002), mice consumed approximately 2 mg doxycycline / day (0.8 mg in chow and 1.2 mg in water). P28 doxycycline treated *K5rtTA;TetOCre;Ift88<sup>fl/fl</sup>* mice or *K5rtTA;TetOCre;Arl13b<sup>fl/fl</sup>* mice and control littermates received an intraperitoneal injection of Methimazole (2-Mercapto-1-methylimidazole, Sigma) (75 mg/kg in sterilized 1xPBS) four weeks after the start of doxycycline diet. Mice were euthanized 8 weeks after methimazole treatment.

*Tissue Collection and Preparation.* Mice were anesthetized with 30% Fluriso (Isoflurane, VetOne), transcardially perfused with 4% paraformaldehyde (PFA), decapitated, and their heads fixed in 4% PFA for 12-16 hours at 4°C. Tissue was then decalcified in 0.5M EDTA (Fisher)/1xPBS overnight at 4°C, cryoprotected in 10% (1hr), 20% (1hr), and 30% sucrose/1xPBS overnight at 4°C, and frozen in OCT compound

(Tissue Tek). 10-12 $\mu$ m of the olfactory epithelium and olfactory bulb were collected on a Leica CM1860 cryostat.

*Immunohistochemistry.* For all immunofluorescence, antigen retrieval was used. For antigen retrieval, tissue sections were rinsed in 1xPBS to remove OCT then incubated in Citrate buffer (pH 6.0) for 30min at 90°C, cooled for 20min at RT, then washed with distilled water for 5min. Sections were blocked with 2% donkey or goat serum, 1% BSA in 1xPBS and incubated overnight in primary antibody. Antibodies were used at the following dilutions: mlgG2a anti-p63 (BioCare Medical, 1:200); mlgG2a anti-ARL13B (Neuromab, 1:500); rabbit anti-ARL13B (Proteintech, 1:500); mlgG1 anti-gamma tubulin (Sigma, 1:500); rabbit anti-K5 (Covance, 1:2500); chicken anti-GFP (Abcam, 1:500); rabbit anti-K18 (Abcam, 1:500); mlgG1 anti-MASH1 (BD Pharmingen, 1:100); mlgG2b anti-SEC8 (BD Transduction Laboratory, 1:500); rabbit anti-LSD1 (Abcam, 1:500); goat anti-OMP (Wako Chemicals, 1:1000); mouse anti-Cre (Millipore, 1:500); mouse anti- $\alpha$  acetylated tubulin (Sigma, 1:1000); rabbit anti-AC3 (EnCor Biotechnology, 1:2000), and rabbit anti-TH (Millipore, 1:500). Sections were washed in 1xPBS three times for 5min each at room temperature and then incubated with Alexa Fluor-conjugated secondary antibodies (1:1000) for 1hr at room temperature. Tissue sections were then incubated with DAPI (Invitrogen, 5mg/ml) for 5 min, washed two times with 1xPBS, and then sealed with cover slips mounted with ProLong Gold (Invitrogen).

For detection of Cre, tissue sections were rinsed in 1xPBS to remove OCT, puddled with citrate buffer, and steamed for 10min in a glass jar in a hot water bath. Sections were blocked with 2% donkey or goat serum/5% dry non-fat milk/4% BSA/1% TTX100 in 1xPBS and incubated overnight in primary antibody. For detection of GFP,

tissue sections were rinsed in 1xPBS to remove OCT, puddled with citrate buffer, and steamed for 10min in a glass jar in a hot water bath. Sections were blocked with 2% donkey or goat serum/0.3% TTX100 in 1xPBS and incubated overnight in primary antibody. For triple staining with MASH1, SEC8, and LSD1 or OMP and Acet-Tub, mouse antibodies or OMP were incubated together overnight and LSD1 or Acet-Tub, respectively, were incubated for 1hr the following day.

*Image processing and quantification.* Images were captured using a Nikon A1R confocal microscope. ImageJ software was used to measure the length of the OE (in  $\mu\text{m}$ ) in each image, to count specific cell types with the cell counter plugin, and to measure the TH intensity. In order to quantify cell types, 10-15 images were taken from the dorsal medial, dorsal lateral, ventral medial, and ventral lateral regions, across 3-4 sections of the OE. Cell counts were averaged and converted to number of cells/mm of OE. Quantitation was performed for N= 3-6 mice in all control, iHBC-IFT88, and iHBC-Arl13b groups, unless otherwise stated. Reported N-values represent the number of mice examined. Measurements of TH intensity were quantified for all glomeruli in each of 3-4 sections of the OB in 4 iHBC-IFT88 and 4 control mice using Image J software. A blind experimental paradigm was utilized to eliminate bias during image processing and quantification.

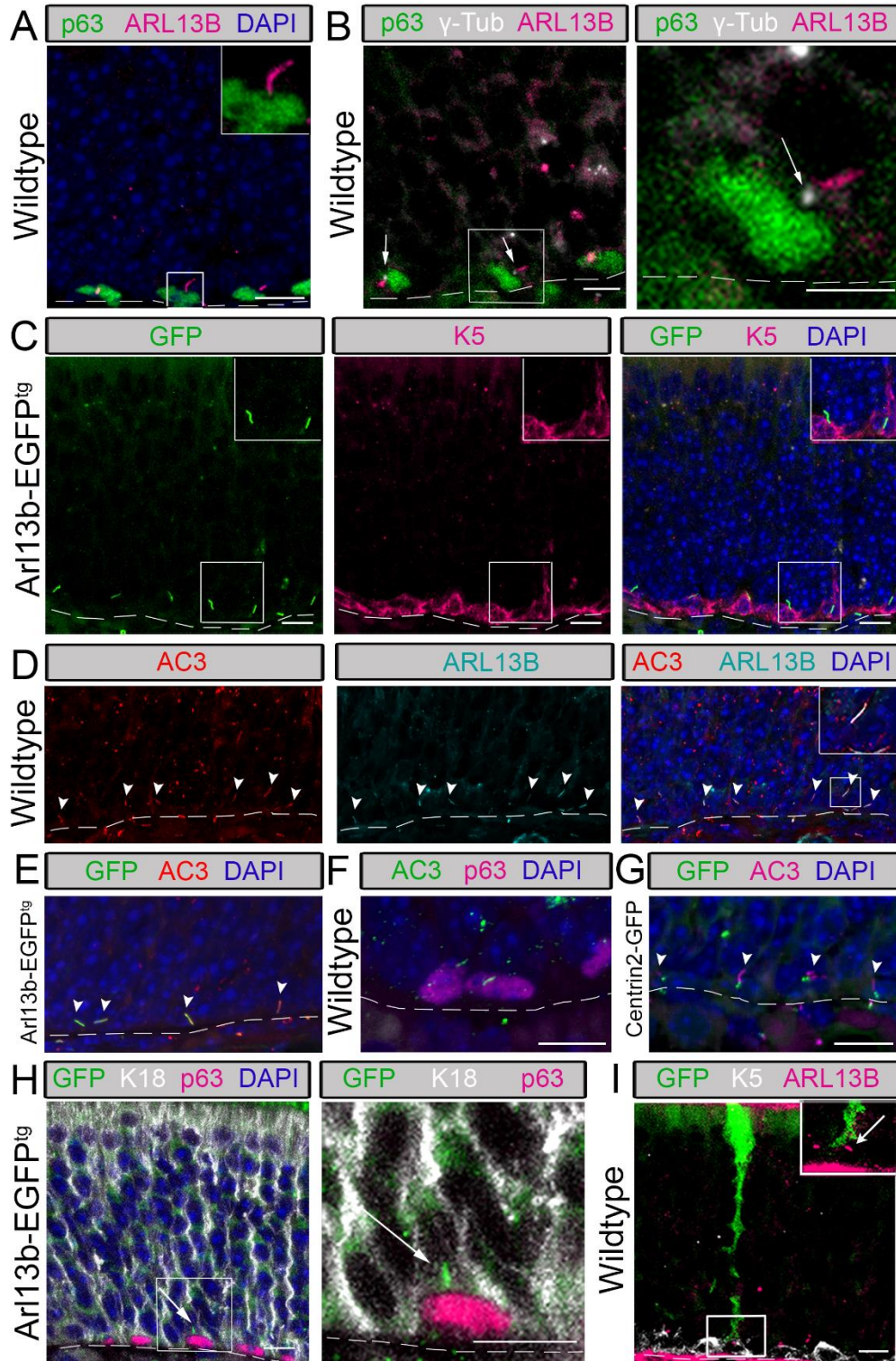
*Statistics.* Statistical significance was determined using an unpaired t test with GraphPad Prism software. Data are presented as mean  $\pm$  SEM with two-tailed P values less than 0.05 considered significant.



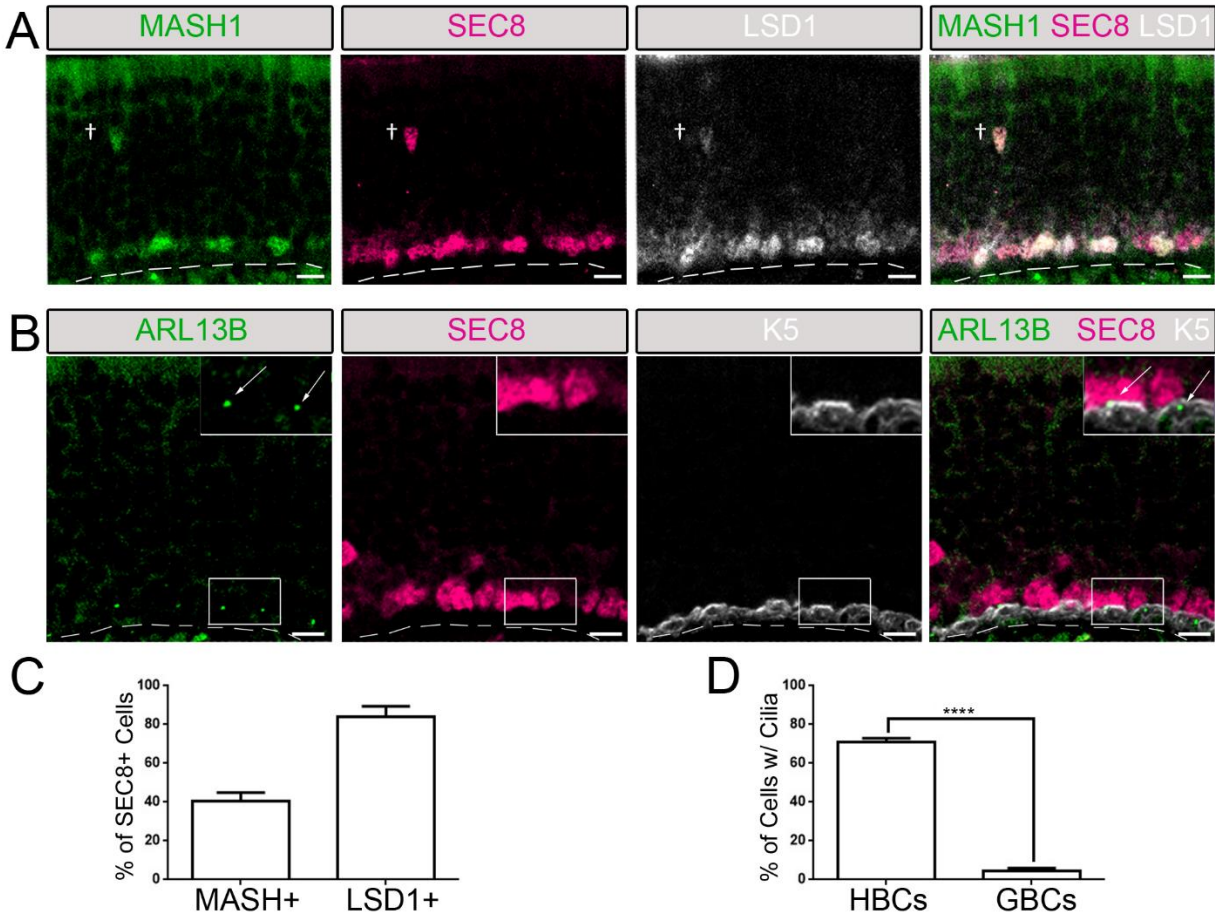
## **2.6 Acknowledgments**

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## 2.7 Figures

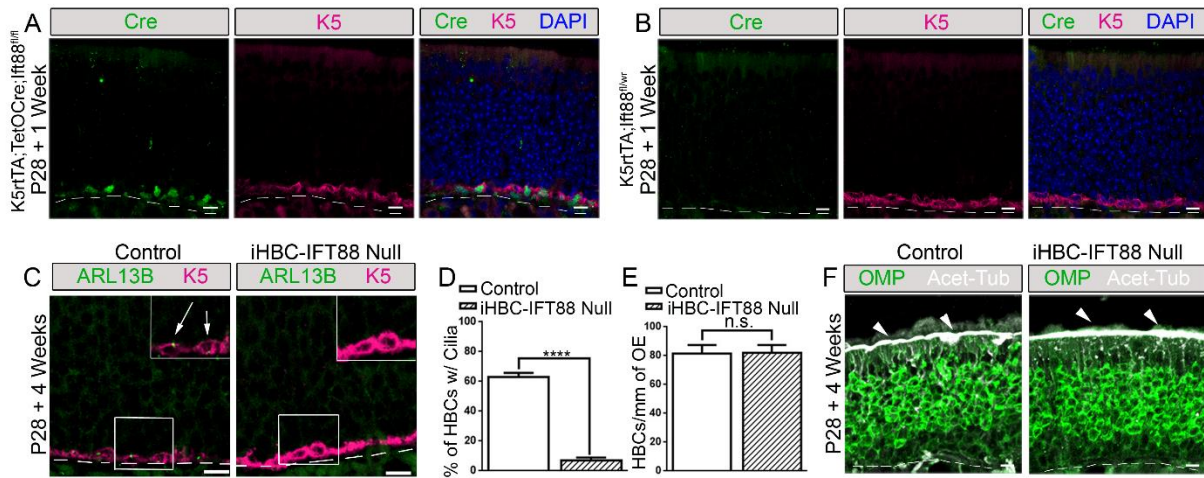


**Figure 2-1. HBCs possess primary cilia.** Immunofluorescence staining was performed on tissue from the olfactory epithelium of 3-6 week old wildtype, *Arl13b-EGFP<sup>tg</sup>*, and *Centrin2-EGFP<sup>tg</sup>* mice. **A**, P63-labeled HBCs possess ARL13B-labeled cilia (inset - magnified image). Scale bars = 10 $\mu$ m. **B**, Cilia extend from gamma ( $\gamma$ ) tubulin-labeled basal bodies (arrows). Low magnification view (left) and high magnification view (right) of ciliated HBC. Scale bars = 5 $\mu$ m. **C**, In *Arl13b-EGFP<sup>tg</sup>* mice, K5-labeled HBCs possess GFP+ cilia (inset – magnified image). Scale bars = 10 $\mu$ m. **D**, HBC cilia labeled with canonical cilia markers Adenylate cyclase III (AC3) and ARL13B. **E**, In *Arl13b-EGFP<sup>tg</sup>* mice, AC3 labels GFP+ cilia. **F**, P63-labeled HBCs possess AC3-labeled cilia. **G**, In *Centrin2-EGFP<sup>tg</sup>* mice, GFP expressing basal bodies possess AC3+ cilia. **H**, In *Arl13b-EGFP<sup>tg</sup>* mice, GFP+ cilia (arrows) project from p63-labeled HBCs into the interstitial space between HBCs and K18-labeled SUS cell endfeet (inset - magnified image. Scale bars = 5 $\mu$ m. **I**, In wildtype mice intranasally infected with adenovirus containing GFP, K5-labeled HBCs possess ARL13B-labeled cilia (see arrow) that project into the interstitial space between an HBC and GFP+ endfoot of a SUS cell (see inset for higher magnified image). Scale bar = 10 $\mu$ m. N=10 total mice for all immunostaining. Dashed lines = basement membrane. HBCs = horizontal basal cells, GFP = green fluorescent protein, K5 = Keratin 5, K18 = Keratin 18, and SUS cells = sustentacular cells.

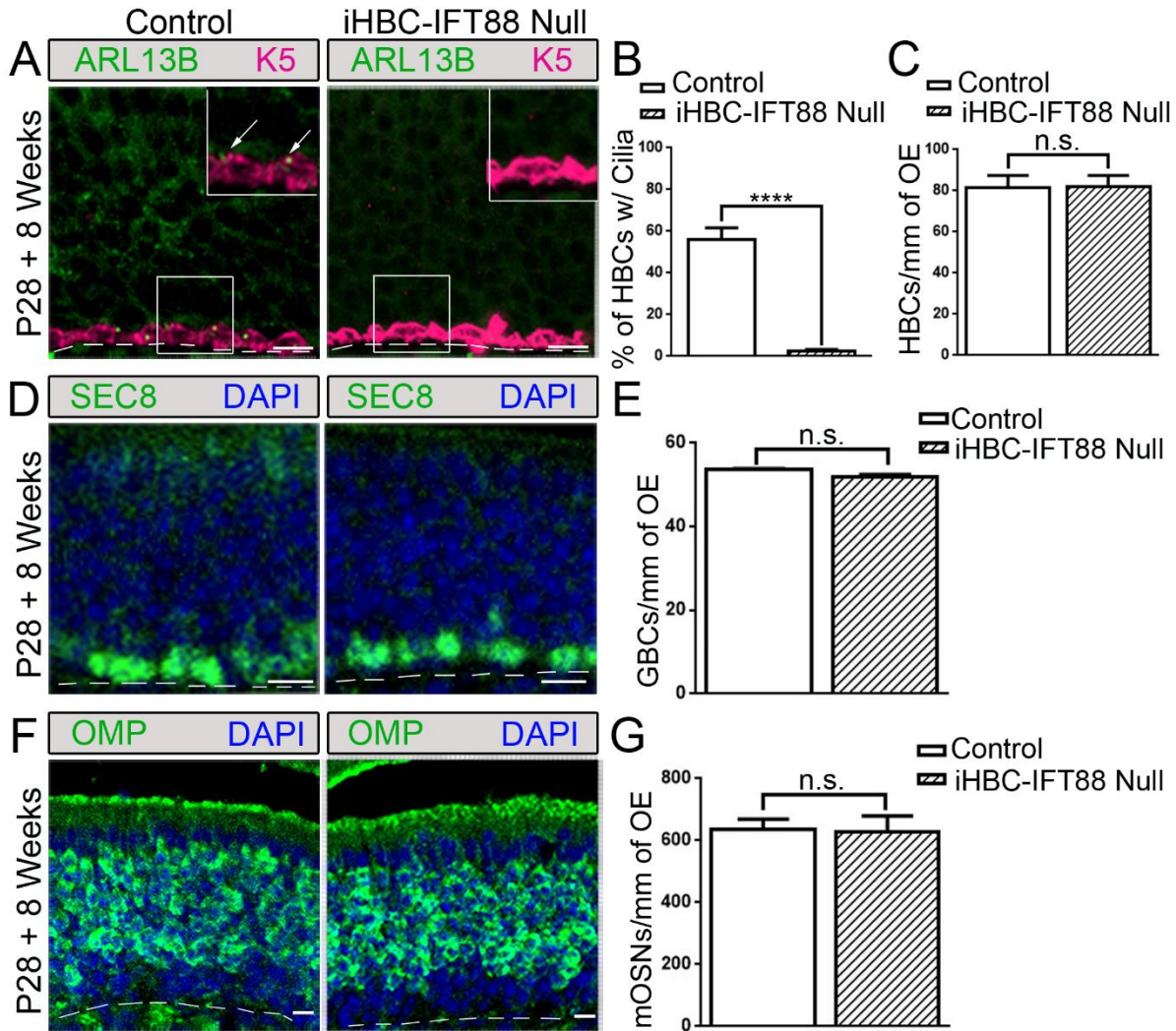


**Figure 2-2. HBCs are the predominantly ciliated olfactory basal stem cell.** Immunofluorescence staining was performed in the olfactory epithelium of wildtype mice. **A**, The canonical GBC marker, MASH1, co-localizes with a subset of SEC8+ GBCs, while, LSD1, co-localizes with a larger subset of SEC8+ GBCs. **B**, Few SEC8-labeled GBCs possess ARL13B-labeled cilia (see arrows) compared to K5-labeled HBCs (inset – magnified image). Scale bars = 10 $\mu$ m. Dashed line = basement membrane. † Occasional migrating GBC. **C**, Quantified data of SEC8+ cells that are either MASH1+ (N=4) or LSD1+ (N=4), and **D**, the percentage of HBCs (N=6) and GBCs (N=6) that possess cilia. \*\*\*\*P<0.0001 by Student *t* test. Data shown are means  $\pm$  SEM. HBCs = horizontal basal cells, GBCs = globose basal cells, and K5 = Keratin 5.

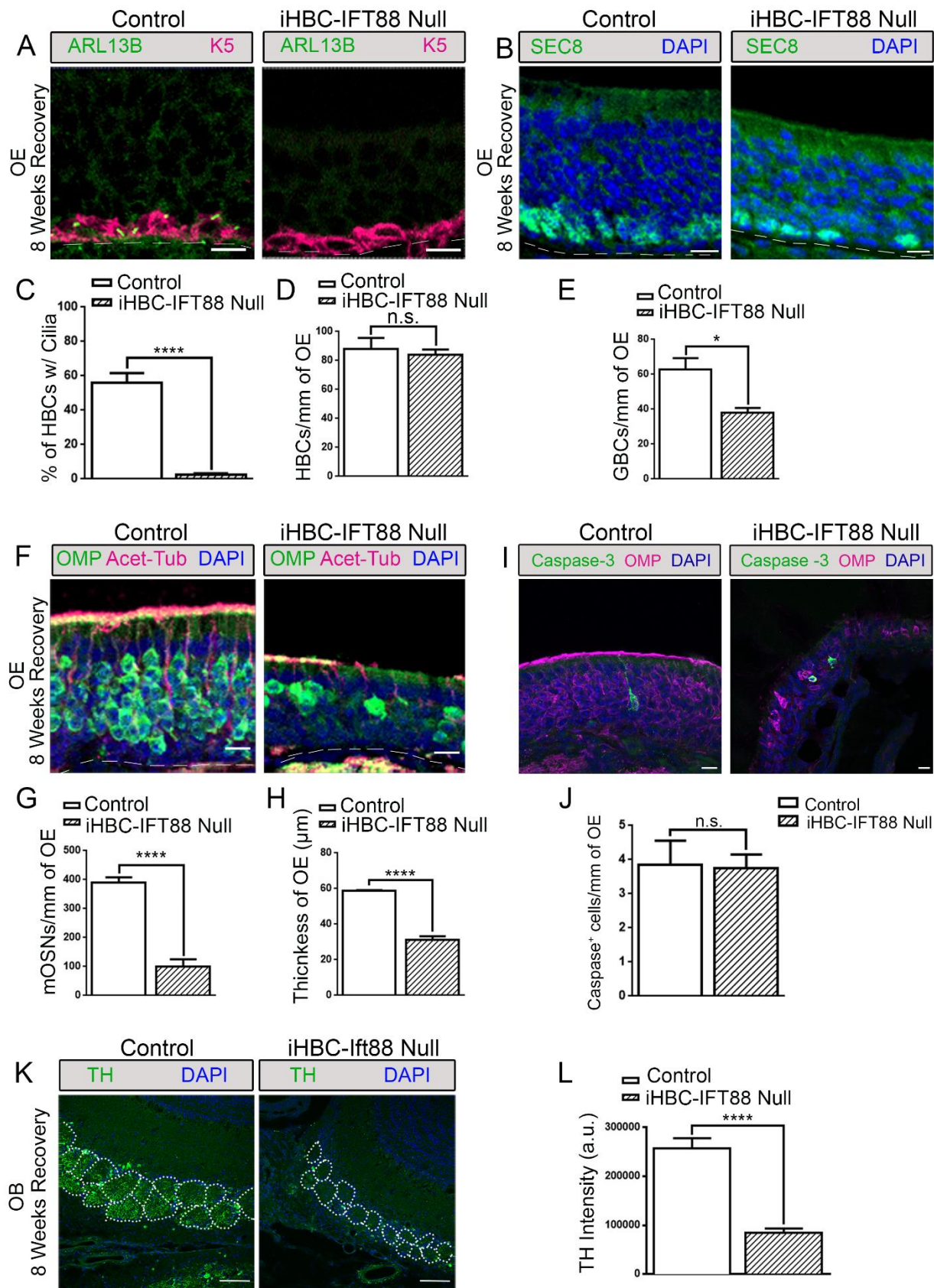




**Figure 2-3. Cell-specific deletion of *Ift88* in HBCs results in the loss of HBC cilia with no effects on OSN cilia.** Control and iHBC-IFT88 mutant mice (referred to as iHBC-IFT88) were administered a doxycycline (dox) diet at postnatal day 28 (P28) for 1 or 4 weeks and immunofluorescence staining of the olfactory epithelium was performed. After 1 week of dox, **A**, Cre is present in K5-labeled HBCs of mice with *K5rtTA* and *TetOCre* alleles but **B**, Cre is absent in mice lacking the *TetOCre* allele. After 4 weeks of dox, **C**, in control mice but not iHBC-IFT88 mice, K5-labeled HBCs possess Arl13b-labeled cilia (see arrows). See inset for higher magnified image. **D**, **E** Quantified data show the percentage of HBCs that are ciliated in control mice is significantly reduced by ~88.5% in iHBC-IFT88 mice with no significant difference in the number of HBCs per mm of OE in control and iHBC-IFT88 mice after 4 weeks of dox. **F**, Acetylated  $\alpha$  tubulin (Acet-Tub)-labeled cilia are still present in OMP-labeled mature OSNs (see short arrows). Scale bars = 10 $\mu$ m. Dashed lines = basement membrane. N=5 for both groups. \*\*\*\*P<0.0001, n.s. = not significant by Student *t* test. Data shown are means  $\pm$  SEM. IFT88 = intraflagellar transport 88, HBCs = horizontal basal cells, cells, OSNs = olfactory sensory neurons, Cre = Cre Recombinase, K5 = Keratin 5, and OMP = olfactory marker protein.



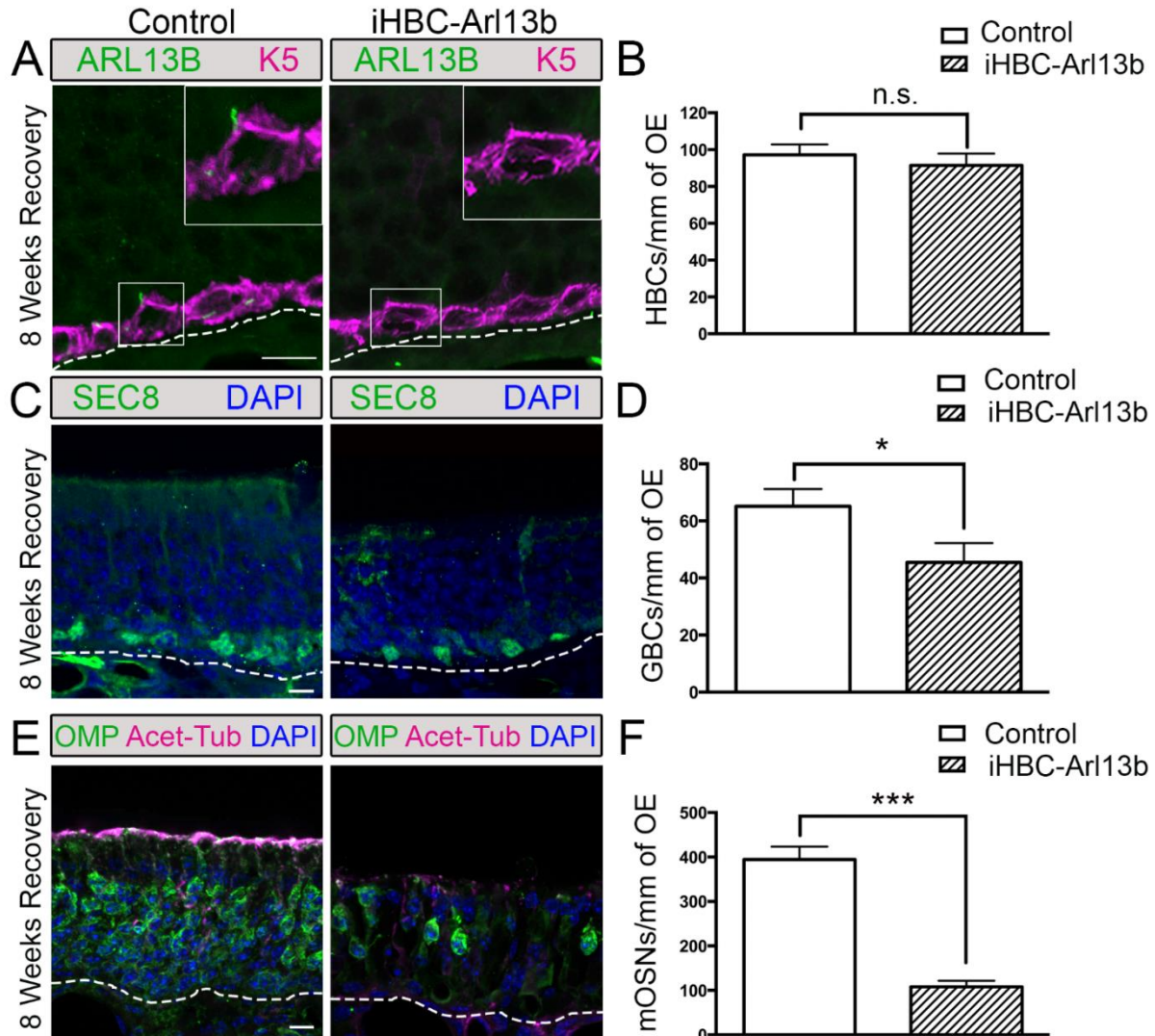
**Figure 2-4. Loss of HBC cilia has no homeostatic effects on the cell composition of the olfactory epithelium (OE).** Control and iHBC-IFT88 mice were administered a doxycycline diet at postnatal day 28 (P28) for 8 weeks. **A**, In control mice, but not iHBC-IFT88 mice, K5-labeled HBCs possess ARL13B-labeled cilia (see arrows) (inset – magnified image). **B**, **C**, Quantified data show a significant loss of ciliated HBCs in iHBC-IFT88 mice with no change in the number of HBCs per mm of OE. **D**, SEC8-labeled GBCs in the OE of control and iHBC-IFT88 mice. **E**, Quantified data show no significant difference in the number of GBCs per mm of OE in both groups. **F**, OMP-labeled mature OSNs in control and iHBC-IFT88 mice. **G**, Quantified data show no significant difference in the number of mature OSNs per mm of OE between both groups. Scale bars = 10 $\mu$ m. Dashed lines = basement membrane. N=2 for control mice and N=4 for iHBC-IFT88 mice. \*\*\*\*P<0.0001, n.s. = not significant by Student *t* test. Data shown are means  $\pm$  SEM. HBC = horizontal basal cells, IFT88 = intraflagellar transport 88, K5 = Keratin 5, GBCs = globose basal cells, OMP = olfactory marker protein, and OSNs = olfactory sensory neurons.



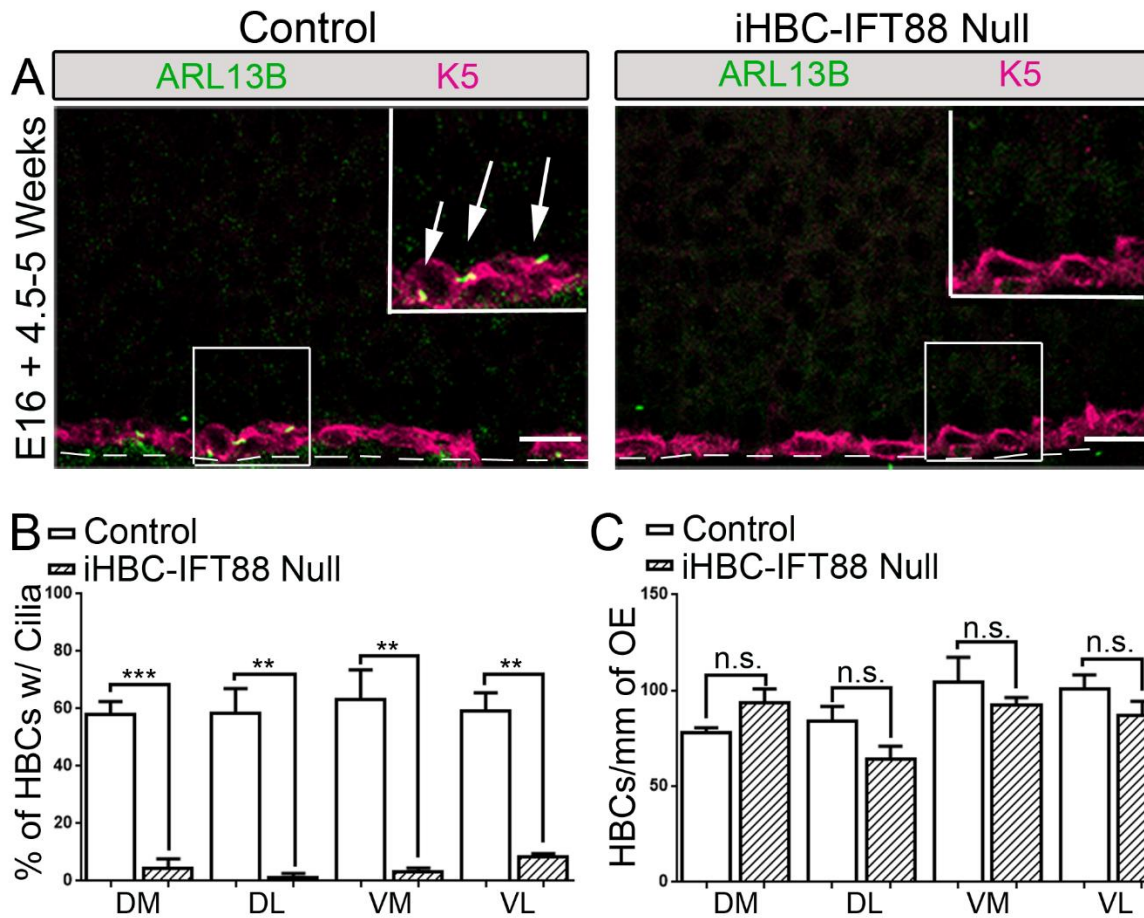


**Figure 2-5. Loss of HBC cilia results in the improper regeneration of the olfactory epithelium (OE) and loss of tyrosine hydroxylase (TH) expression in the olfactory bulb (OB).** Control and iHBC-IFT88 mice were administered a doxycycline (dox) diet at postnatal day 28 (P28) for 4 weeks and then given an intraperitoneal injection of 75mg/kg of Methimazole to ablate the OE. Following 8 weeks of recovery, immunofluorescence staining was performed. **A**, In the OE of control mice but not iHBC-IFT88 mice, K5-labeled HBCs possess ARL13B-labeled cilia. **B**, SEC8-labeled GBCs in the OE of control and iHBC-IFT88 mice. **C-D**, Quantified data show the percentage of HBCs that are ciliated in control mice is significantly reduced in iHBC-IFT88 mice with no difference in the number of HBCs per mm of OE between both groups. **E**, Quantified data show a significant reduction in the number of GBCs per mm of OE. **F**, OMP-labeled mature OSNs and acetylated  $\alpha$  tubulin (Acet-Tub)-labeled cilia in the OE of control and iHBC-IFT88 mice. **G**, Quantified data show a significant reduction in the number of mature OSNs per mm of OE, and **H**, a significantly thinner OE in iHBC-IFT88 mice. **I - J**, No difference in the number of cleaved caspase-3 labeled apoptotic cells was observed in the OE of control and iHBC-IFT88 mice. **K**, TH expression within glomeruli (dotted circles) in the OBs of control and iHBC-IFT88 mice. **L**, Quantified data show that the intensity of TH measured in arbitrary units is significantly reduced in the OBs of iHBC-IFT88 mice. Scale bars = 10 $\mu$ m. Dashed lines = basement membrane. N=4 for both groups. \*P<0.05, \*\*\*\*P<0.0001, n.s. = not significant by Student *t* test. Data shown are means  $\pm$  SEM. HBCs = horizontal basal cells, IFT88 = intraflagellar transport 88, K5 = Keratin 5, GBCs = globose basal cells, OMP = olfactory marker protein, and OSNs = olfactory sensory neurons.

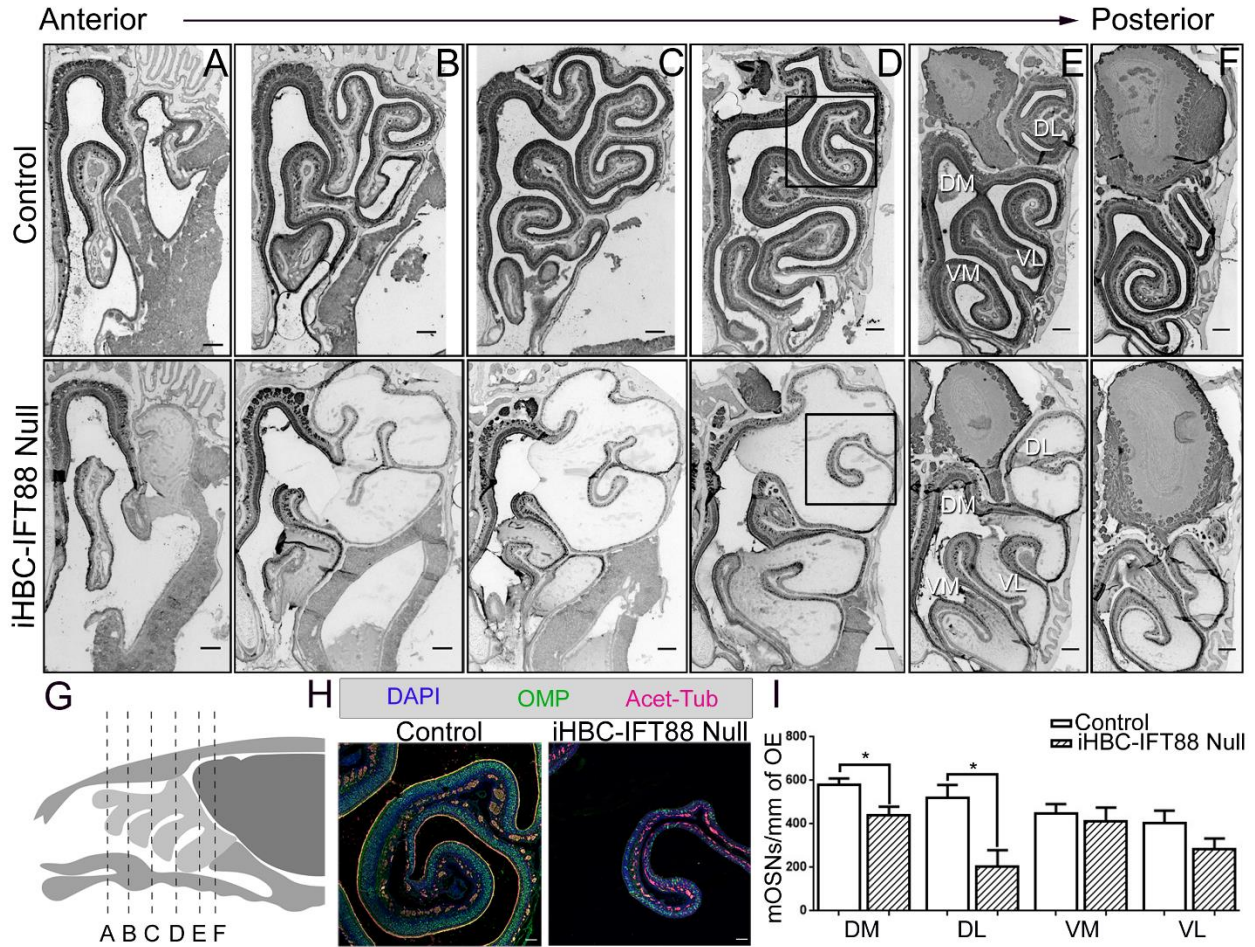




**Figure 2-6. Loss of *Arl13b* in HBCs results in the improper regeneration of the olfactory epithelium (OE).** Control and iHBC-ARL13B mice were administered a doxycycline diet at postnatal day 28 for 4 weeks to induce deletion of *Arl13b*. Mice were then given an intraperitoneal injection of 75mg/kg of methimazole to ablate the OE and allowed 8 weeks of recovery. **A**, K5-labeled HBCs in the OE of iHBC-ARL13B mice do not possess ARL13B-labeled cilia. **B**, The percentage of HBCs per mm of OE in both control and iHBC-ARL13B mice. **C**, SEC8-labeled GBCs in the OE of control and iHBC-ARL13B mice. **D**, Quantified data show a significant reduction in the number of GBCs per mm of OE. **E**, OMP-labeled mature OSNs and acetylated  $\alpha$  tubulin (Acet-Tub)-labeled cilia in the OE of control and iHBC-ARL13B mice. **F**, Quantified data show a significant reduction in the number of mature OSNs per mm of OE. Scale bars = 10µm. Dashed lines = basement membrane. N=3 for both groups. \*P<0.05, \*\*\*P<0.001, n.s. = not significant by Student *t* test. Data shown are means  $\pm$  SEM. HBCs = horizontal basal cells, ARL13B = ADP-ribosylation factor-like protein 13b, K5 = Keratin 5, GBCs = globose basal cells, OMP = olfactory marker protein, and mOSNs = mature olfactory sensory neurons.

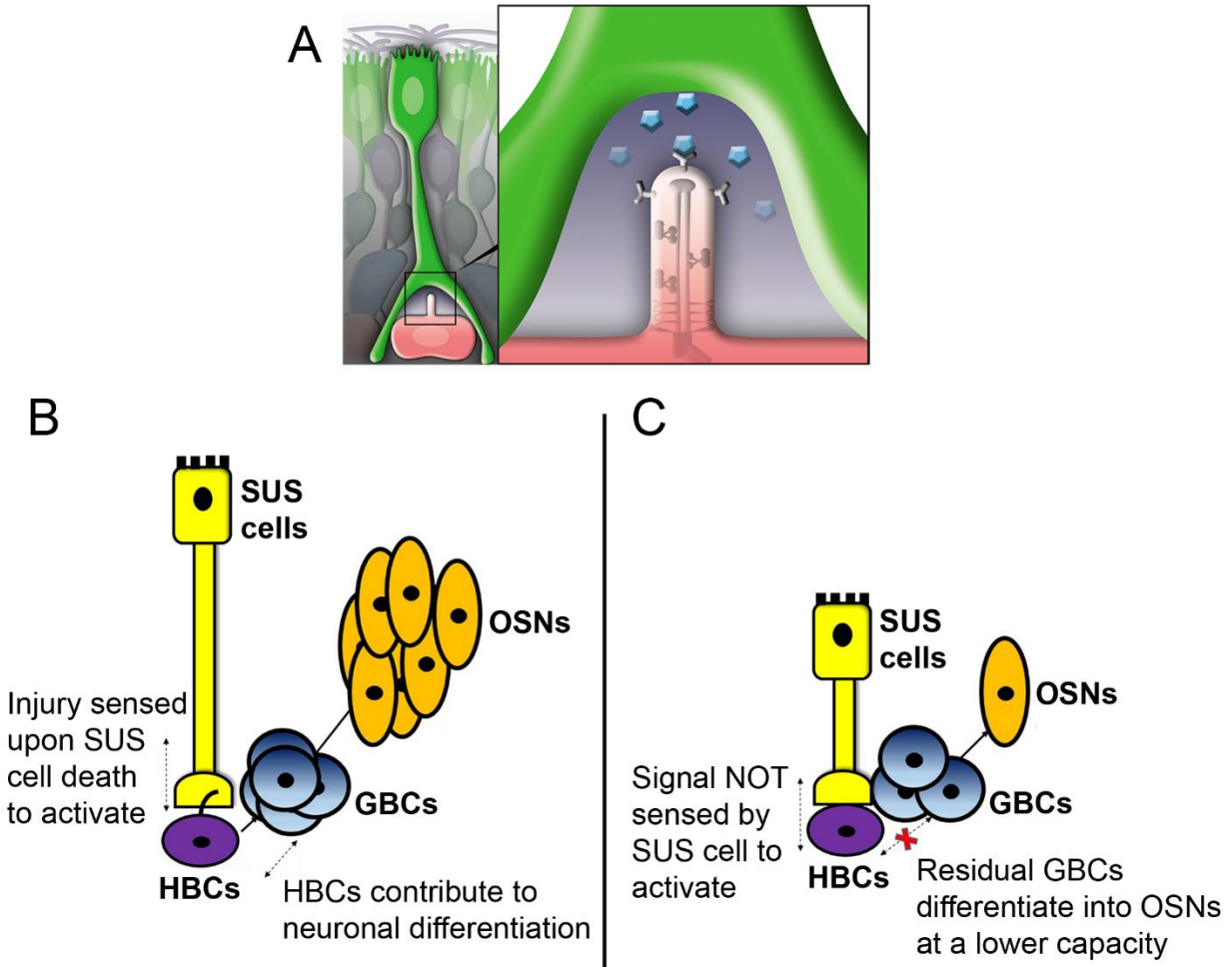


**Figure 2-7. Conditional deletion of *Ift88* in HBCs during development of the olfactory epithelium (OE) results in the loss of HBC cilia with no effects on the number of HBCs.** Control and iHBC-IFT88 null mice were treated with doxycycline at embryonic day 16 (E16) for 4.5-5 weeks and analyzed at postnatal day 28 (P28) with immunofluorescence staining of the OE. **A**, In control mice, but not iHBC-IFT88 null mice, K5-labeled HBCs possess ARL13B-labeled cilia (see arrows) (inset - magnified image). Scale bars = 10 $\mu$ m. Dashed lines = basement membrane. Quantified data show **B**, the percentage of HBCs that are ciliated in control mice is significantly reduced in iHBC-IFT88 null mice across all regions and **C**, the number of HBCs per mm of OE is similar across all regions in both groups. N=3 for both groups. \*\*P<0.01, \*\*\*P<0.001, n.s. = not significant by Student *t* test. Data shown are means  $\pm$  SEM. HBCs = horizontal basal cells, IFT88 = intraflagellar transport 88, K5 = Keratin 5, DM = dorsal medial, DL = dorsal lateral, VM = ventral medial, and VL = ventral lateral.



**Figure 2-8. Loss of HBC cilia results in the impaired development of regions in the olfactory epithelium (OE).** Control and iHBC-IFT88 mice were treated with doxycycline at embryonic day 16 (E16) for 4.5-5 weeks and analyzed at postnatal day 28 (P28) with immunofluorescence staining of the OE. **A-F**, OMP-labeled mature OSNs in anterior to posterior sections of control and iHBC-IFT88 mice. Scale bars = 200 $\mu$ m. **G**, Illustration depicting the location of sections A-F in a sagittal view of the mouse olfactory organ. **H**, Magnified view of boxed region in **D** with OMP-labeled mature OSNs and acetylated  $\alpha$  tubulin (Acet-Tub)-labeled cilia in the OE of control and iHBC-IFT88 mice. Scale bars = 50 $\mu$ m. **I**, Quantified data show the number of mature OSNs per mm of OE in iHBC-IFT88 mice is significantly reduced specifically in dorsal lateral and medial regions of the OE but not in ventral regions. N=5 for both groups. \*P<0.05 by Student *t* test. Data shown are means  $\pm$  SEM. HBCs = horizontal basal cells, IFT88 = intraflagellar transport 88, OMP = olfactory marker protein, OSNs = olfactory sensory neurons, DM = dorsal medial, DL = dorsal lateral, VM = ventral medial, and VL = ventral lateral.





**Figure 2-9. Model of HBC cilia-dependent neurogenesis during restoration and development of the olfactory epithelium (OE).** **A**, Illustration shows that the SUS endfoot may release some signal factor that is received and transduced by HBC cilia. **B**, Following an injury, when HBCs possess cilia, SUS cells alert HBCs to the lesion resulting in their activation and production of additional GBCs, which contribute to regeneration of OSNs. **C**, Without cilia, HBCs no longer detect a signal from SUS cells, resulting in limited recovery from residual GBCs and a thinner OE. HBCs = horizontal basal cells, SUS cells = sustentacular cells, GBCs = globose basal cells and OSNs = olfactory sensory neurons.

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## CHAPTER III:

### Role of Hedgehog Signaling in the Adult Mammalian Olfactory Epithelium

#### 3.1 Abstract

The olfactory epithelium (OE) is a pseudostratified tissue composed of various cell types including olfactory sensory neurons (OSNs) that are readily replaced by two populations of basal stem cells, frequently dividing globose basal cells (GBCs) and quiescent horizontal basal cells (HBCs). This continuous replacement of OSNs makes the OE one of the few tissues to undergo constitutive neurogenesis throughout the mammalian lifespan. Although the cell types involved in the maintenance and regeneration of the OE are known, the signaling pathways that control their activation and proliferation during normal homeostasis, and in response to injury remain largely unexplored. Previous data indicate that HBCs possess primary cilia (Joiner and Green, et. al., submitted), cellular organelles that regulate the activity of multiple signaling pathways, including the Hedgehog (HH) signaling pathway. The HH pathway is implicated in stem and progenitor cell function in several adult tissues, making it an attractive candidate for the regulation of HBCs. Here, I show that various components of the HH pathway are expressed in cells of the OE. Specifically, I found that the HH transcription factors, GLI2 and GLI3 are expressed in HBCs, suggesting that HH signaling is involved in regulation of HBCs. To test this hypothesis, I utilized two inducible, cell-type specific

mouse models (Fig. 3-1): 1) a constitutively active form of *Gli2* (*K5-rtTA;TetO-Gli2ΔN*) and 2) a dominant negative repressive form of *Gli2* (*K5-rtTA;TetO-Gli2ΔC4*) to disrupt HH signaling specifically in HBCs. The constitutive activation of *Gli2* in HBCs resulted in their hyperproliferation and consequential loss of neuronal cells and also impaired regeneration of the OE following lesion. Interestingly, the repressive form of *Gli2* in HBCs did not affect the maintenance of the adult OE but led to a decrease in regeneration following an injury. Together, these results suggest a novel role for HH and more specifically, *Gli2*, in HBC regulation and HBC-driven neurogenesis.

## 3.2 Introduction

The olfactory epithelium (OE) is a tissue of regeneration and constitutive neurogenesis (Graziadei and Graziadei, 1979; Graziadei and Monti Graziadei, 1983; Calof and Chikaraishi, 1989). Olfactory sensory neurons (OSNs) within the OE act as a direct link between the CNS and the external environment (Doty, 2008), causing them and other cells to be susceptible to various injuries resulting from inhalation of toxicants or metabolism of drugs (Hastings and Miller, 2003; Murphy et al., 2003). Fortuitously, two groups of presumed stem cells: globose basal cells (GBCs) and horizontal basal cells (HBCs) (Murdoch and Roskams, 2007) are able to replenish the OSNs and other non-neuronal cells in the OE. *In vitro* studies and fate-mapping studies in rodents have shown the varying differentiation pathways of HBCs and GBCs under specific conditions. Although in defined conditions HBCs can generate multiple differentiated neuronal and glial progeny *in vitro* (Carter et al., 2004), GBCs were initially thought to be the main contributor to regeneration of the OE (Treloar et al., 2010). However, in more recent fate-mapping studies, in which GBCs are depleted from a severe injury to the OE, HBCs were shown to be multipotent stem cells that can regenerate neuronal and non-neuronal cells (Leung et al., 2007; Iwai et al., 2008).

HBCs and GBCs have distinct characteristics and expression profiles. HBCs lie in a monolayer against the basement membrane of the OE. They are a quiescent, homogeneous population of cells (Holbrook et al., 1995; Carter et al., 2004; Leung et al., 2007) that were recently found to possess primary cilia that were necessary for proper regeneration of the OE following a severe injury (Joiner et al., 2015). GBCs are a heterogeneous population of cells situated just above HBCs and below immature OSNs

(Packard et al., 2011a; Krolewski et al., 2013). Among the GBCs are transit-amplifying progenitor cells and committed neuronal precursors (Jang et al., 2014). During neurogenesis in the OE, a subset of GBCs that are *Ascl1+* (*Mash1+*) transit amplifying cells primarily give rise to *Neurogenin1+* (*Ngn1+*) and *NeuroD1+* immediate neuronal precursors (Duggan et al., 2008; Krolewski et al., 2013), and a recent study suggests that a subpopulation of GBCs are also multipotent progenitors that likely give rise to non-neuronal cells (Jang et al., 2014).

Various growth factors and pathways have been reported to play a role in the proliferation and differentiation of basal stem cells (reviewed in Murdoch and Roskams, 2007). In particular, Notch (Manglapus et al., 2004; Krolewski et al., 2012) and Wnt (Chen et al., 2014) are suggested to play a role in the differentiation of GBCs; however, these studies did not use direct *in vivo* models to perturb specific components of the pathways. The recent finding of cilia on HBCs and its role in regeneration of the OE reveals new potential signaling pathways that could be involved in the regulation of HBCs and neurogenesis in the OE.

Primary cilia are cellular organelles that regulate the activity of multiple signaling pathways, including the HH signaling pathway (for review, see ref. Nozawa et al., 2013). In other tissues, primary cilia have important roles in cell proliferation and cell differentiation (for review, see ref. Irigoien and Badano, 2011). The HH pathway is not only important for the development of various tissues and organs but also for the formation, survival, and function of stem and progenitor cell populations in several adult tissues (reviewed in Petrova and Joyner, 2014). Additionally, there is growing evidence that adult stem cells utilize cilia for adult neurogenesis (Amador-Arjona et al., 2011; Kumamoto et

al., 2012; Tong et al., 2014). In particular, disruption of cilia in these systems alters the activity of signaling pathways that utilize cilia, such as HH (Kumamoto et al., 2012; Tong et al., 2014). Canonical HH signaling occurs through a signal transduction cascade mediated by the GPCR-like protein smoothed (SMO) following ligand binding to the canonical HH receptor patched 1 (PTCH1), resulting in modulation of the downstream GLI transcription factors (Chen and Struhl, 1996; Ingham et al., 2000; Fan et al., 2012). In the absence of ligand, PTCH1 suppresses SMO activity, allowing for GLI3, and to a lesser extent GLI2, to be processed into transcriptional repressors; following HH binding to PTCH1, SMO enters the cilium and promotes the processing of GLI2 into a transcriptional activator and the degradation of GLI3 (for review, see ref. Petrova and Joyner, 2014). Due to its utilization of cilia and the fact that cilia regulate HBC-driven neurogenesis in the OE, the HH pathway is an attractive candidate for the regulation of HBCs. However, the HH pathway remains largely unexplored in the mammalian OE (Chou et al., 2010). Interestingly, a study reported that the HH target gene, *Pax6* (Briscoe et al., 2000), is expressed in HBCs and is essential for the differentiation of HBCs into neuronal cells during regeneration following an MMI-induced injury to the OE (Suzuki et al., 2015), suggesting a potential role for HH signaling in OE maintenance.

Here, I show that components of the HH pathway are expressed in distinct cell populations in the OE, suggesting a potential role for the pathway in olfactory tissue maintenance. Specifically, HBCs express the transcription factors GLI2, and GLI3, suggesting a role for the HH pathway in the molecular regulation of olfactory basal stem cells in the OE. Following expression of a constitutively active form of GLI2 (GLI2 $\Delta$ N) (Fig. 3-1) in HBCs of mice, HBCs become hyperproliferative with an upregulation of the GBC

marker, SEC8, and a consequential loss of neuronal cells. Additionally, there is incomplete regeneration of the OE following an injury. Conversely, HBC-specific expression of a dominant-negative GLI2 repressor (GLI2 $\Delta$ C4) (Fig. 3-1) does not change the cell types of the OE during normal tissue homeostasis; however, there is a reduction in regeneration and neurogenesis following an injury. These data identify expression of HH pathway components in specific cells of the OE, implicating a previously unrecognized pathway (HH) in the regulation of OE homeostasis. Additionally, these data provide mechanistic insight into the regulation of HBCs during olfactory regeneration, and indicate a potential role for HH signaling in the differentiation of HBCs during neurogenesis.

### 3.3 Results

*HH components are found in cells of the olfactory periphery.*

The HH pathway is an attractive candidate for the regulation of HBCs due to its dependence on primary cilia in tissue maintenance (Croyle et al., 2011). However, in the mammalian olfactory epithelium (OE), a potential role for the HH pathway remains largely unexplored (Gong et al., 2009). To investigate if components of the HH pathway were present in the OE, I analyzed the heads of *lacZ* reporter mice with an X-Gal stain to read out expression of the specific transcript of interest (Fig. 3-2). Tissue from these mice was incubated with an X-Gal substrate that is cleaved by  $\beta$ -Galactosidase, producing a blue precipitate that indicates *lacZ* expression. Compared to control tissue in which no color is present (Fig. 3-2A-C'''), sagittal views of the whole mouse head indicate that most core HH pathway components are found throughout various regions of the brain, including the



cerebellum (Fig. 3-2D, G, J, M). Interestingly, *Gli1*, a general readout of HH activity (Lee et al., 1997) is not expressed in the olfactory bulb (OB) (Fig. 3-2E) and only faintly detected in the olfactory turbinates (bony structures that are comprised of OE) specifically in the stroma (Fig. 3-2F'-F'''). *Gli2*, the common transcriptional activator of the HH pathway (Matisse et al., 1998; Pan et al., 2006), is expressed in the dorsal part of the OB (Fig. 3-2H) and throughout all olfactory turbinates in more ventral and anterior areas (Fig. 3-2I'-I'''). The major transcriptional repressor of the HH pathway, *Gli3* (Litingtung and Chiang, 2000; Wang et al., 2000), is not detected in the OB (similar to *Gli1*; Fig. 3-2K) but is detected in the OE more faintly, but in a similar pattern to *Gli2* (Fig. 3-2L'-L'''). Conversely, the HH receptor, *Ptch1*, which, like *Gli1*, is a direct target of the pathway and reads out HH pathway activity (Agren et al., 2004), is expressed throughout the OB (Fig. 3-2N) and in more dorsal and posterior areas of the olfactory turbinates (Fig. 3-2O'-O'''). The expression profiles of these HH pathway components are unusual, especially because *Gli1* and *Ptch1*, which are typically expressed together, do not appear to have the same expression profile in the olfactory turbinates. Interestingly, the expression profile of *Gli2* is typical of the profile of a repressor of the pathway in which the profile is in opposition to the expression profile of *Ptch1* (Goodrich et al., 1996; Marigo and Tabin, 1996; Ruiz i Altaba, 1998). These data demonstrate that HH components are expressed not only in the CNS, but also in the olfactory periphery.

To analyze the expression profile of the HH components more closely, coronal sections of the *lacZ* reporter mice were obtained and incubated with X-Gal substrate (Fig. 3-3). Again, no color developed in control tissue (Fig. 3-3A-D). Similar to the whole mount images (Fig.3-2), *Gli1* is not expressed in the OE, but instead in cells within the underlying

Lamina Propria (LP) (Fig. 3-3E-H). *Gli2* is expressed in basal cells of the OE (Fig. 3-3I-L) and, in some areas, detected in apical cells that appear to be SUS cells (Fig. 3-3L). Similarly, *Gli3* is also expressed in basal cells (Fig. 3-3M-P) and a subset of SUS cells (3-3N, P), but with less intensity and uniformity than *Gli2*. In contrast, *Ptch1* is strongly expressed in a region-specific and “patchy” pattern in apical cells that appear to be OSNs, and possibly at a lower intensity in basal cells (Fig. 3-3Q-T). Together, these results corroborate the whole mount images in Figure 3-2, and also suggest that HH pathway components are expressed in distinct cell types within the mammalian OE.

*HH pathway components are present in distinct cell populations of the olfactory epithelium.*

In order to confirm the cell types in the OE that express specific HH pathway components, I performed a sequential X-Gal and immunofluorescence stain on tissue from *Gli2<sup>lacZ/+</sup>*, *Gli3<sup>lacZ/+</sup>*, and *Ptch1<sup>lacZ/+</sup>* mice. Following incubation with the X-Gal substrate, I immunolabeled the OE with either the recently identified marker of GBCs, SEC8 (Joiner and Green, et. al., submitted), and the HBC marker, Keratin 5 (K5) (Holbrook et al., 1995), or the immature OSN marker, growth-associated protein 43 (GAP-43) (McIntyre et al., 2010) and the mature OSN marker, olfactory marker protein (OMP) (McIntyre et al., 2010). Dual staining revealed that *Gli2* is expressed in all K5+ cells but excluded from SEC8+ cells (Fig. 3-4A), while *Gli3* is present in a subset of K5+ cells but not in SEC8+ cells (Fig. 3-4B). Additionally, I found that *Ptch1* is expressed in OMP+ cells but not in GAP-43+ cells or in more basally located cells (Fig. 3-4C). *Ptch1* expression was thought to be present at a lower intensity in immature OSNs and basal cells based on X-Gal staining in sections of the OE (Fig 3-3Q-T), however, it is possible that this low

signal was not resolved in the dual staining. Nonetheless, these data suggest that *Gli2* and *Gli3* are expressed selectively in HBCs of the OE, while *Ptch1* is expressed in a region-specific manner in mature OSNs.

*Constitutively active Gli2 in HBCs results in proliferative HBCs.*

GLI2 contains both transcriptional activation and repression domains and therefore, full-length GLI2 is a weak transcriptional activator (Sasaki et al., 1999). Deletion of the N-terminal repression domain results in Gli2 protein that functions as a strong transcriptional activator (Gli2 $\Delta$ N) in cultured cells and mimics overactive SHH signaling in transgenic mice (Sasaki et al., 1999). In order to investigate the role of GLI2 as a transcriptional activator in HBCs, I analyzed *K5-rtTA;TetO-Gli2 $\Delta$ N* mice (Grachtchouk et al., 2011) which utilize a doxycycline (dox)-regulated mouse model (Gunther et al., 2002). These mice carry two alleles: 1) a promoter specific dox-inducible strain (*K5-rtTA*) (Diamond et al., 2000) and 2) an effector strain (*tetO-Gli2 $\Delta$ N*) (Grachtchouk et al., 2011). The *K5* promoter drives expression of the reverse tetracycline transactivator (rtTA) and binding of doxy to rtTA allows for binding to the tetracycline operator (tetO) and expression of *Gli2 $\Delta$ N* specifically in HBCs in the OE.

*K5-rtTA;TetO-Gli2 $\Delta$ N* mice (referred to hereafter as iHBC-Gli2 $\Delta$ N mice) and control littermates (referred to hereafter as control mice) were initially administered a dox diet to activate Gli2 $\Delta$ N expression in HBCs after P28, when the OE is mature (Murdoch and Roskams, 2007). Mice were treated with dox for 24 hours, 3 days, 5 days, 7 days, or 10 days. Antibody staining for the HBC markers, p63 and K5, revealed that, compared to control mice (Fig. 3-5A1), which exhibit a typical monolayer of HBCs (Holbrook et al., 1995), there is initially no difference in the appearance and number of HBCs in iHBC-

Gli2 $\Delta$ N mice after 24 hours (Fig. 3-5AII, B) and 3 days (Fig. 3-5AIII, B). However, following 5 days of dox treatment, HBCs undergo a change in morphology as they become more round and GBC-like in appearance (Fig. 3-5AIV). By 7 and 10 days, the population of HBCs has expanded and are no longer a monolayer of cells (Fig. 3-5AV-AVI). This change in appearance following 5 days of dox is reflected in the doubling, and eventual tripling by 10 days, of the number of HBCs (Fig. 3-5B). Consequently, the increase in the number of HBCs, results in an increase in thickness of the HBC layer (Fig. 3-5C). These data suggest that constitutively active GLI2 causes a switch of the HBCs from a dormant state to an active state. When the transcription factor, p63, is downregulated, HBCs are believed to be activated and differentiate into other cell types (Packard et al., 2011a). However, the additional HBCs seen in iHBC-Gli2 $\Delta$ N mice still express p63 (Fig. 3-5AV-AVI).

In order to determine the proliferative state of the HBCs in these mice, I utilized the antibody Ki67 which should label cells in the G1, S, and G2 phase of the cell cycle but not in quiescent cells in the G0 phase (Scholzen and Gerdes, 2000). Staining the OE of iHBC-Gli2 $\Delta$ N and control mice after 10 days of dox with Ki67 and p63 revealed that, compared to controls, in which Ki67 is excluded from p63+ HBCs, iHBC-Gli2 $\Delta$ N mice display an overall increase in Ki67+ cells which are also p63+ (Fig. 3-5D-E). Typically, HBCs do not express Ki67+ due to their quiescence, but in iHBC-Gli2 $\Delta$ N mice, approximately 40% of p63+ HBCs express Ki67. Together, these data suggest that constitutively active GLI2 induces HBC proliferation leading to a morphological and quantitative change. These findings further suggest that: 1) active HH signaling promotes

HBC proliferation of HBCs, and 2) p63 downregulation is required for subsequent HBC differentiation.

*GLI2 localizes to tips of proliferative HBC primary cilia.*

The *Gli2 $\Delta$ N* transgene contains a MYC tag, allowing for its detection and the localization of GLI2 protein (Grachtchouk et al., 2011). As detailed in Chapter II, HBCs possess primary cilia (Joiner and Green, et. al., submitted) and GLI2 protein localizes to the tips of primary cilia in many HH-responsive tissues (Haycraft et al., 2005; Liu et al., 2005). In order to investigate when and where GLI2 $\Delta$ N protein was expressed, I immunolabeled the OE of iHBC-Gli2 $\Delta$ N and control mice with MYC and ARL13B, a small Ras GTPase that regulates ciliogenesis and cilia function and labels HBC cilia (Joiner et al., 2015). After 24 hours of dox treatment, although I did not see a change in HBCs (Fig. 3-5AII, B), MYC is present in approximately 70% of HBCs in iHBC-Gli2 $\Delta$ N mice but not in control mice (Fig. 3-6A-B). By 7 days of dox, nearly 90% of HBCs in iHBC-Gli2 $\Delta$ N mice express MYC but not in control mice (Fig. 3-6A-B). Interestingly, MYC is present in only 5% of HBC primary cilia in iHBC-Gli2 $\Delta$ N mice after 24 hours of dox, while MYC is present in nearly 20% of HBC primary cilia in iHBC-Gli2 $\Delta$ N mice following 7 days of dox (Fig. 3-6C). These data suggest a correlation between the presence of GLI2 protein in primary cilia and subsequent HBC proliferation. Additionally, to determine if Gli2 $\Delta$ N localized specifically to the tips of HBC primary cilia, I stained the OE with the basal body marker gamma ( $\gamma$ ) tubulin in addition to ARL13B and MYC. This staining revealed that MYC was present in HBC primary cilia on opposite ends of the  $\gamma$ -tubulin+ basal bodies (Fig. 3-5D). These data demonstrate that Gli2 $\Delta$ N does localize to the tips of primary cilia in HBCs.

*Constitutively active Gli2 in HBCs results in SEC8 upregulation and loss of neuronal cells in the OE.*

To determine the status of other cells in the OE following an atypical proliferation of HBCs not triggered by an injury, I analyzed the neuronal GBC and OSN populations of HBC-Gli2 $\Delta$ N mice. As previously mentioned, SEC8 labels a majority of the heterogeneous population of GBCs (Joiner and Green, et. al., submitted). Surprisingly, analysis of p63+ HBCs and GBCs immunolabeled with SEC8 revealed that although control mice contain a typical layer of SEC8+ GBCs above a monolayer of p63+ HBCs, iHBC-Gli2 $\Delta$ N mice after 5 and 10 days of dox contain cells co-expressing SEC8 and p63 (Fig. 3-7A). The overall number of SEC8+ cells increases in iHBC-Gli2 $\Delta$ N mice after 5 and 10 days of dox (Fig. 3-7B). The percentage of p63+ HBCs that express SEC8, which is 0% in control mice, increases to 60% and 90% of HBCs after 5 and 10 days of dox respectively (Fig. 3-7C). These data suggest that SEC8 is upregulated in the HBCs of iHBC-Gli2 $\Delta$ N mice and that activation of GLI2 mediates this upregulation.

Although SEC8, labels a majority of GBCs, there are other markers for neuronal committed GBCs such, as MASH1 (Cau et al., 1997). The number of MASH1+ GBCs in the OE of iHBC-Gli2 $\Delta$ N mice was dramatically decreased after 5 and 10 days of dox compared to control mice (Fig. 3-8A-B). Since all MASH1+ cells are also SEC8+ (Joiner and Green, et. al., submitted), any remaining MASH1+ cells in HBC-Gli2 $\Delta$ N mice could be indicative of SEC8+ cells that do not co-express p63 (Fig. 3-7C). Additionally, GAP-43+ immature OSNs and OMP+ mature OSNs are both reduced in iHBC-Gli2 $\Delta$ N mice compared to control mice after 5 days of dox (Fig. 3-8C-D). Together, these data indicate that hyperproliferation of HBCs results in a loss of neuronal cells in the OE and suggest

the need for HBC quiescence to be tightly regulated, possibly mediated by *Gli2* expression in HBCs.

*Constitutively active Gli2 in HBCs results in improper regeneration of the olfactory epithelium following injury.*

HBCs are believed to be a quiescent population of cells unless activated by severe injury to participate in OE regeneration (Leung et al., 2007). Methimazole (MMI) is an olfactory toxicant whose metabolites induce cell death of OSNs, SUS cells, and GBCs but spares HBCs in the mouse OE (Brittebo, 1995; Packard et al., 2011b). MMI injury to the OE is used to study the response of HBCs during restoration of the OE. Due to the lethality of iHBC-Gli2 $\Delta$ N mice after prolonged dox treatment, I induced the injury after 5 days of dox, when a phenotype in HBCs was seen, and looked at early recovery time points (2 days, 5 days, and 9 days). Importantly, mice continued the dox diet during the recovery period. On the day of the injury, but after 5 days of dox (Day 0), iHBC-Gli2 $\Delta$ N mice have an increased number of p63+/K5+ HBCs that are no longer restricted to a monolayer of cells as seen in control mice (Fig. 3-9A, E). Control mice contain an increased number of K5+/p63+ inactive HBCs and K5+/p63- active HBCs at 2 days following an injury, while iHBC-Gli2 $\Delta$ N mice continue to have an even greater number of both active and inactive HBCs (Fig. 3-9B, E-F). By 5 days following injury, the appearance and number of HBCs of control mice have returned to normal while iHBC-Gli2 $\Delta$ N mice still display an increased number of K5+/p63+ inactive and K5+/p63- active HBCs (Fig. 3-9C, F-G). HBCs are no longer active at 9 days following injury in control mice, but the number of inactive and active HBCs is dramatically increased in iHBC-Gli2 $\Delta$ N mice (Fig. 3-9D, F-G). Overall, in control mice, the number of active HBCs appears to peak 2 days

after injury and then decreases over time in control mice, while the number of active and inactive HBCs continues to increase in iHBC-Gli2 $\Delta$ N mice (Fig. 3-9F-G). These data suggest that HBCs in iHBC-Gli2 $\Delta$ N mice are still able to become active to replenish HBC numbers, but that they remain in a fixed active state that cannot go on to differentiate into other cells of the OE.

To determine whether other cells in the OE are replaced by the activation and differentiation of HBCs, I immunolabeled the OE of the same mice with the neuronal GBC marker, MASH1, immature OSN marker, GAP-43, and mature OSN marker, OMP. After 5 days of dox, and at the time of injury (Day 0), iHBC-Gli2 $\Delta$ N mice contain decreased numbers of MASH1+ GBCs (Fig. 3-10A, I), as well as GAP-43+ immature and OMP+ mature OSNs (Fig. 3-9B, J-K) compared to control mice. Following 2 days of recovery, both control and iHBC-Gli2 $\Delta$ N mice exhibit a decrease in the number of MASH1+ GBCs (Fig. 3-10C, I) and immature and mature OSNs (Fig. 3-10D, J-K). By 5 days following injury, in control mice, MASH1+ GBCs return and are greater in number than prior to injury but are still nearly absent in iHBC-Gli2 $\Delta$ N mice (Fig. 3-10E, I). Additionally, immature OSNs have returned with very few mature OSNs in control mice, while both populations of cells are absent in iHBC-Gli2 $\Delta$ N mice (Fig. 3-10F, J-K). The number of MASH1+ GBCs returns to normal by 9 days of recovery in control mice, but are absent in iHBC-Gli2 $\Delta$ N mice (Fig. 3-10G, I). Similarly, the number of immature OSNs increases in control mice by 9 days after injury with an additional return of mature OSNs, while iHBC-Gli2 $\Delta$ N mice continue to show no return of immature or mature OSNs (Fig. 3-10H, J-K). These data suggest that constitutive GLI2 activation in HBCs impairs their ability to contribute to regeneration of the OE.



*Dominant negative repressive Gli2 in HBCs does not alter OE homeostasis.*

To investigate the repressive effects of GLI2 on HBCs, I utilized a dominant negative form of GLI2, *Gli2 $\Delta$ C4*, in which the activation domain in the C-terminus is truncated (Sasaki et al., 1999). Similar to iHBC-*Gli2 $\Delta$ N* mice, I used *K5-rtTA;TetO-Gli2 $\Delta$ C4* mice which were generated in the laboratory of Dr. Andrzej Dlugosz at the University of Michigan (unpublished), which utilize the same dox-regulated model. However, in addition to the promoter specific dox-inducible strain (*K5-rtTA*) (Diamond et al., 2000), these mice carry the effector strain (*tetO-Gli2 $\Delta$ C4*) which was generated in the laboratory of Dr. Dlugosz. The *K5* promoter drives expression of the reverse tetracycline transactivator (rtTA) and binding of doxy to rtTA allows for binding to the tetracycline operator (tetO) and expression of *Gli2 $\Delta$ C4* specifically in HBCs in the OE.

*K5-rtTA;TetO-Gli2 $\Delta$ C4* mice (referred to hereafter as iHBC-*Gli2 $\Delta$ C4* mice) and control littermates (referred to hereafter as control mice) survive longer than iHBC-*Gli2 $\Delta$ N* mice; therefore, mice were treated with a dox diet for a longer period of time. Additionally, HBCs are typically quiescent and the constitutively active form of GLI2 promoted proliferation, so I hypothesized that dominant negative GLI2 would not acutely affect OE homeostasis. Therefore, iHBC-*Gli2 $\Delta$ C4* mice and control mice were treated with dox for 36 days and tissue was immunolabeled with p63 and K5 to analyze HBCs, or MASH1 and SEC8 to analyze GBCs. Strikingly, the appearance and number of HBCs (Fig. 3-11A, C) and GBCs (Fig. 3-11B, D) in iHBC-*Gli2 $\Delta$ C4* and control mice were not significantly different. Although, I was unable to detect the transgene in HBCs due to inadequate antibodies, I observed obvious skin and tail phenotypes in iHBC-*Gli2 $\Delta$ C* mice, suggesting that the transgene is expressed in *K5*-expressing cells of the skin. These data indicate

that the repressive form of GLI2 does not affect OE homeostasis, which suggests that the HH pathway is either normally inactive or functions mainly as a repressor in the adult OE.

*Dominant negative Gli2 repressor expression in HBCs results in improper OE regeneration following injury.*

To explore whether GLI2 must be active in HBCs for basal cells to contribute to OE regeneration, I again utilized MMI injury to the OE of iHBC-Gli2 $\Delta$ C4 mice. GLI2 $\Delta$ C4 should be the dominant form of GLI2 expressed in the HBCs of these mice. Because these mice survive longer on dox (compared to GLI2 $\Delta$ N animals), I analyzed the OE 8 weeks following injury when the OE should be nearly fully recovered (Genter et al., 1995; Bergman and Brittebo, 1999). I initially induced the *Gli2* $\Delta$ C4 transgene with a dox diet for 7 days which continued throughout the recovery period.

At Day 0 of injury and 8 weeks following injury, iHBC-Gli2 $\Delta$ C4 and control mice have a similar number of p63+/K5+ HBCs (Fig. 3-12A, C). The number of SEC8+ GBCs at Day 0 is unchanged in iHBC-Gli2 $\Delta$ C4 compared to control mice however at 8 weeks post injury, there is a decrease in the number of SEC8+ GBCs (Fig. 3-12B, D), suggesting a decrease in the differentiation of HBCs into GBCs. Furthermore, while there are no differences in the number of OSNs at Day 0 of injury, after 8 weeks of recovery, there is a decrease in the number of GAP-43+ immature OSNs and OMP+ mature OSNs (Fig. 3-12E-G). Interestingly, there is not a complete loss of neurons and the OSNs that do return appear in a regionally variable manner. Together, these data suggest that dominant negative GLI2 repressor impairs HBC-driven OE regeneration and that HBCs require GLI2 activation to ensure normal OE regeneration.

*Gli2 regulation of SEC8 during the HBC to GBC transition in OE regeneration.*

Many of the transcription factors expressed in GBCs, including *Mash1* and *Ngn*, are necessary for OSN development (Cau et al., 1997; Cau et al., 2002). SEC8 is a secretory protein that is thought to be involved in exocytosis acting as a targeting protein for exocytosis or secretion of various proteins (Friedrich et al., 1997). Its loss results in incomplete gastrulation and embryonic lethality (Friedrich et al., 1997). Interestingly, *Sec8* null embryos like *Mash1* null mice, display a loss of *Notch1* (Friedrich et al., 1997; Cau et al., 2002), which is thought to play an important role in GBC differentiation (Manglapus et al., 2004).

I showed that iHBC-Gli2 $\Delta$ N mice exhibit an upregulation of SEC8 in HBCs while iHBC-Gli2 $\Delta$ C4 mice have a normal expression profile of SEC8 seen only in GBCs. These observations suggest that the active form of GLI2 is necessary for the HBC to GBC transition of HBCs. To test this hypothesis, I analyzed the expression of p63, K5, and SEC8 in the OE of iHBC-Gli2 $\Delta$ N mice that had been induced with an MMI injury to the OE. On Day 0 of the injury (5 days of dox), iHBC-Gli2 $\Delta$ N mice contain increased numbers of p63+/K5+ HBCs and increased numbers of SEC8+ cells that have been upregulated in these HBCs (Fig. 3-13A, E). There is a further increase in SEC8+ cell numbers in iHBC-Gli2 $\Delta$ N mice 2 days following injury, while control mice show a slight decrease (Fig. 3-13B, E). By 5 days following injury, control mice display increased numbers of SEC8+ cells, while there is a slight decrease in iHBC-Gli2 $\Delta$ N mice (Fig. 3-13C, E). The number of SEC8+ cells remains normal at 9 days following injury in control mice, but are dramatically increased in iHBC-Gli2 $\Delta$ N mice (Fig. 3-13D, E). Further analysis of SEC8 expression in either inactive or active cells reveals that: 1) SEC8 is upregulated in a majority of inactive HBCs in the iHBC-Gli2 $\Delta$ N mice regardless of injury, but only in a small

percentage in control mice soon after injury (Fig. 3-13F), 2) SEC8 is expressed in active HBCs of both control and iHBC-Gli2 $\Delta$ N mice following injury (Fig. 3-13G), and 3) SEC8 remains upregulated in the active HBCs in iHBC-Gli2 $\Delta$ N mice, while in control mice, SEC8 is eventually downregulated (Fig. 3-13G). Together these data suggest that GLI2 upregulates SEC8 in HBCs for them to become active but GLI2 must be downregulated to allow for HBCs to differentiate into SEC8+/p63- GBCs (Fig. 3-14).

### 3.4 Discussion

The HH pathway plays important roles in embryonic development and in adult tissue homeostasis and neurogenesis (reviewed in Petrova and Joyner, 2014). Here, I provide evidence that HH pathway components are expressed in distinct cell populations in the OE. Interestingly, the transcription factor, *Gli1*, which is a transcriptional readout of the HH pathway and often co-expressed with *Ptch1* (Lee et al., 1997; Agren et al., 2004) is absent from the OE. Because *Gli1* expression is dependent on *Gli2* and *Gli3* (Bai et al., 2004) and *Gli1*<sup>-/-</sup> mice are viable (Park et al., 2000), GLI2 and GLI3 are believed to be the primary transcriptional effectors of HH signaling, while *Gli1* is presumably secondarily activated at the transcriptional level (Sasaki et al., 1999). Therefore, it is possible that GLI1 does not function in the OE, especially if GLI2 and GLI3 act as repressors of the pathway in HBCs, which would preclude GLI1 expression in HBCs. However, different HH pathway components could be upregulated or downregulated in response to OE injury. Particularly, it would be interesting to visualize the expression of *Gli2* transcript following an MMI injury to determine whether *Gli2* downregulation correlates with the HBC to GBC transition. Analysis of *lacZ* reporter mice that are induced with an MMI injury could

verify this concept. Although *Gli* transcripts are present in various cell types of the OE, I do not have information about their corresponding protein levels due to inefficient antibodies. Furthermore, because GLI2 and GLI3 act as both transcriptional activators and repressors (Buttitta et al., 2003), it is important to understand how they are processed in both the normal OE and the injured OE. Future work to analyze GLI protein modifications and levels would help elucidate how these transcription factors function in HBCs.

My data indicate that HBC-specific expression of constitutively active GLI2 promotes hyperproliferation and a subsequent loss of neuronal cells and impaired regeneration. Constitutively active GLI2 as well as full-length GLI2 can drive tumorigenesis, and when expressed in epidermal basal cells of mice, they form tumors characteristic of human basal cell carcinomas (Grachtchouk et al., 2000; Grachtchouk et al., 2011). Interestingly a subset of follicle stem cells are resistant to Gli2 $\Delta$ N-mediated tumorigenesis, suggesting that there may be cell-specific protective mechanisms in place. In the OE, HBC proliferation is not uniform which could suggest a protective mechanism or could be due to timing of transgene induction. Interestingly, newly formed HBCs in iHBC-Gli2 $\Delta$ N mice still possess primary cilia, which is not indicative of a proliferative cell (Plotnikova et al., 2009). However, my previous work indicates that the loss of HBC cilia does not stimulate proliferation (Joiner and Green, et. al., submitted), suggesting that these cells may not be as tightly regulated to the cell cycle as other cells. GLI2 trafficking to cilia is necessary for its processing (Haycraft et al., 2005; Humke et al., 2010; Tukachinsky et al., 2010). Additionally, GLI2 transcriptionally activates *cyclin D1* and *cyclin D1*, which function in G1 phase of the cell cycle to promote cell cycle progression

(Mill et al., 2003). It is possible that there is a correlation between the presence of GLI2 in the cilia of HBCs and their proliferative status. Understanding the correlation between proliferative HBCs and ciliated HBCs as well as the presence of GLI2 in primary cilia could provide more insight into the role of primary cilia in the cell cycle regulation of HBCs.

What remains unknown is the fate of neuronal cells that are lost as a consequence of HBC proliferation. If the OE has an intrinsic maximum capacity for the number of cells it can withstand, it is possible that the neuronal cells die at the expense of newly formed HBCs. Analyzing apoptosis in the OE at various time points of dox treatment would confirm what happens to these cells. Additionally, after MMI-induced injury, I observed incomplete regeneration of the OE in iHBC-Gli2 $\Delta$ N mice, apparently due to a lack of HBC differentiation, which instead appear fixed in an intermediate state. HBCs normally differentiate and replenish the GBC population following injury (Leung et al., 2007; Iwai et al., 2008). In iHBC-Gli2 $\Delta$ N mice, SEC8 expression, which is regulated by GLI2 appears to be associated with the transition from HBCs to GBCs. However, *Gli2* transcript is not present in SEC8+ GBCs (Fig. 3-4A), suggesting that the expression of SEC8 might only need transient *Gli2* expression for it to be transcriptionally activated. In control mice, SEC8 is upregulated to a lesser extent earlier in the recovery period (Fig. 3-13B-C, F-G), in support of the idea that GLI2 is processed as an activator transiently during regeneration. Analyzing GLI2 transcript and protein following an MMI injury would determine what is seen in its upregulation or downregulation following injury. Although there are no studies that investigate the relationship between SEC8 and GLI2, there are reports on the relationship between GLI2 and the HBC marker and transcription factor, p63. In osteosarcoma cells, p63 induces *Gli2* expression by binding to the *Gli2* promoter,

suggesting that *Gli2* is a direct transcriptional target of p63 (Ram Kumar et al., 2014). Normally, downregulation of p63 is associated with activation and differentiation of HBCs into other cells of the OE following an injury. Furthermore, p63 is thought to act as a promoter of HBC cell renewal and inhibit its differentiation (Fletcher et al., 2011). However, in iHBC-*Gli2* $\Delta$ N mice, despite downregulation of p63 leading to HBC activation, HBCs do not differentiate. Since *Gli2* is a target of p63, when p63 is downregulated, *Gli2* should also be downregulated, but in iHBC-*Gli2* $\Delta$ N mice potentially this downregulation cannot occur leading HBCs to stay in a fixed intermediate HBC/GBC state. Future work investigating the role of SEC8 in this process and whether SEC8 is a direct transcriptional target of *Gli2* would help elucidate the mechanisms controlling HBC differentiation.

As mentioned previously, GLI2 normally functions as an activator and GLI3 as a repressor of the HH pathway, but there are some instances where they can have reverse roles (Buttitta et al., 2003; Bai et al., 2004). Interestingly, expression of dominant negative GLI2 repressor (GLI2 $\Delta$ C4) did not alter HBC function in the OE of iHBC-*Gli2* $\Delta$ C4 mice during normal tissue homeostasis (Fig. 3-12). However, following an MMI-induced injury these mice exhibited a loss of neurogenesis and regeneration of the OE (Fig. 3-12). These data suggest that GLI2 is processed into a repressor in HBCs in order to maintain their quiescence and upon injury, must be differentially processed into an activator to initiate HBC-driven neurogenesis. Without GLI2 activator function, HBCs are stuck in a quiescent state and are therefore unable to contribute to regeneration of the OE. Because *Gli3* is expressed in a subset of HBCs (Fig. 2-4B), it is also possible that *Gli3* can act as a transcriptional activator. Following injury, GLI3 processing to an activator would initiate HBC activation. Analyzing *Gli3* transcript and GLI3 protein levels following injury as well

as the proliferation of HBCs at early time points during recovery in iHBC-Gli2 $\Delta$ C4 mice would be useful in further understanding the dynamics of GLI protein function in the OE. Additionally, analysis of a loss of *Gli2* (Corrales et al., 2006) and/or *Gli3* (Blaess et al., 2008) in HBCs using conditional mouse models would elucidate the repressive or activator roles these transcription factors play in regulation of HBCs and neurogenesis and if any redundancies are present.

Finally, an important HH pathway component that is missing in the OE is HH ligand. There are three different HH ligands in the mammalian HH signaling pathway, DHH, IHH, and SHH (Echelard et al., 1993). I was unable to definitively determine which HH ligands are present in the OE and where they are expressed. Due to the proximity of SUS cells and GBCs to HBCs and their cilia, the ligand source could be present in these cells. SUS cells extend projections that terminate in endfeet that contact HBCs via HBC primary cilia (Joiner and Green, et. al., submitted). Importantly, there are examples of ligand-independent HH signaling, specifically in cancer (Onishi et al., 2011; Lei et al., 2013). If HH ligand is not present in the OE, the regulation of HBCs could be occurring in a ligand-independent manner. Future work to look at inhibition of the HH pathway via a SMO inhibitor (Low and de Sauvage, 2010) or complete loss of SMO using conditional mouse models (Long et al., 2001) could provide more insight on whether the regulation of HBCs is ligand-dependent or independent.

In conclusion, the expression of HH pathway components in the OE, specifically in HBCs, and their importance in tissue homeostasis and neurogenesis reveals a potentially novel role for HH signaling in the OE, provides insight into a possible GLI-dependent and



repressive role for HH signaling during homeostasis, and defines a novel mechanism involved in the regulation of olfactory basal stem cells.

### 3.5 Materials and Methods

*Mouse strains and Genotyping.* All mice were maintained on a mixed genetic background. Transgenic *K5-rtTA;TetO-Gli2 $\Delta$ N* (Grachtchouk et al., 2011) and *K5-rtTA;TetO-Gli2 $\Delta$ C4* mice (unpublished) were provided by Dr. Andrzej Dlugosz (University of Michigan). All mice of either sex were housed and maintained according to the University of Michigan and University of Florida institutional guidelines. All protocols for mouse experimentation were approved by the University of Michigan Committee on the Use and Care of Animals. Genotyping was performed using primers and PCR parameters from previously published work referenced above.

*Doxycycline Transgene Induction and olfactory epithelium lesion.* Mice were administered doxycycline water (200 $\mu$ g/ml doxycycline, 5% sucrose, Fisher) for the first 3 days of treatment and fed doxycycline chow (1g/kg doxycycline, Bio-Serv) from the beginning of treatment after postnatal day 28 (P28) until the time of euthanasia. Based on an approximate daily food intake of 4 g/mouse and water intake of 6ml/mouse (Bachmanov et al., 2002), mice consumed approximately 2 mg doxycycline / day (0.8 mg in chow and 1.2 mg in water). Dox treated *K5-rtTA;TetO-Gli2 $\Delta$ N* mice or *K5-rtTA;TetO-Gli2 $\Delta$ C4* mice and their control littermates received an intraperitoneal injection of Methimazole (2-Mercapto-1-methylimidazole, Sigma) (75 mg/kg in sterilized 1xPBS) five days or 7 days after the start of dox diet respectively. *K5-rtTA;TetO-Gli2 $\Delta$ N* mice were

euthanized 2, 5, or 9 days after MMI treatment while *K5-rtTA;TetO-Gli2ΔC4* mice were euthanized 8 weeks after MMI treatment.

*Tissue Collection and Preparation.* Mice were anesthetized with 30% Fluriso (Isoflurane, VetOne), transcardially perfused with 4% paraformaldehyde (PFA), decapitated, and their heads fixed in 4% PFA for 12-16 hours at 4°C. Tissue was then decalcified in 0.5M EDTA (Fisher)/1xPBS overnight at 4°C, cryoprotected in 10% (1hr), 20% (1hr), and 30% sucrose/1xPBS overnight at 4°C, and frozen in OCT compound (Tissue Tek). 10-12μm of the olfactory epithelium and olfactory bulb were collected on a Leica CM1860 cryostat.

*X-Gal staining.* Tissue sections were rinsed in 1xPBS to remove OCT and then incubated in X-gal solution for 6 hours at 37°C. Sections were rinsed in 1xPBS to remove X-gal solution, incubated in Nuclear Fast Red (Sigma) for 5min at RT, rinsed in water, and rinsed in 75% EtOH, 95% EtOH, 100% EtOH, and Xyelens for 5min each. After drying, sections were sealed with cover slips mounted with Permount (Fisher).

*Immunohistochemistry.* For all immunofluorescence, antigen retrieval was used. For antigen retrieval, tissue sections were rinsed in 1xPBS to remove OCT then incubated in Citrate buffer (pH 6.0) for 30min at 90°C, cooled for 20min at RT, then washed with distilled water for 5min. Sections were blocked with 2% donkey or goat serum, 1% BSA in 1xPBS and incubated overnight in primary antibody. Antibodies were used at the following dilutions: mlgG2a anti-p63 (BioCare Medical, 1:200); mlgG2a anti-ARL13B (Neuromab, 1:500); rabbit anti-ARL13B (Proteintech, 1:500); mlgG1 anti-gamma tubulin (Sigma, 1:500); rabbit anti-K5 (Covance, 1:2500); mlgG1 anti-MASH1 (BD Pharmingen, 1:100); mlgG2b anti-SEC8 (BD Transduction Laboratory, 1:500); goat anti-OMP (Wako

Chemicals, 1:1000); rabbit anti-GAP-43 (Millipore, 1:500); rabbit anti-Ki67 (Abcam, 1:500); and rabbit anti-MYC (Abcam, 1:500). Sections were washed in 1xPBS three times for 5min each at room temperature and then incubated with Alexa Fluor-conjugated secondary antibodies (1:1000) for 1hr at room temperature. Tissue sections were then incubated with DAPI (Invitrogen, 5mg/ml) for 5 min, washed two times with 1xPBS, and then sealed with cover slips mounted with ProLong Gold (Invitrogen).

For dual X-Gal and Immunofluorescence staining, tissue sections first underwent an X-Gal stain as described above, but instead of incubation in Nuclear Fast Red, sections were puddled with citrate buffer, and steamed for 10min in a glass jar in a hot water bath. Sections were then blocked and stained as described in the immunohistochemistry section above.

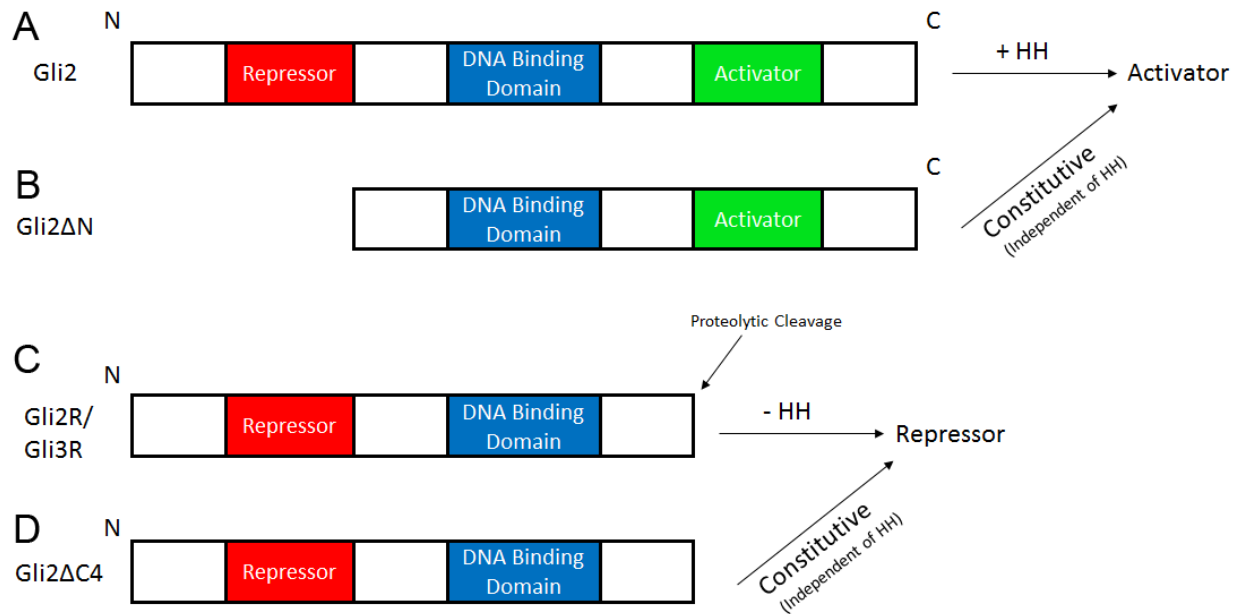
*Image processing and quantification.* Images were captured using a Nikon A1R confocal microscope. ImageJ software was used to measure the length of the OE (in  $\mu\text{m}$ ) in each image and to count specific cell types with the cell counter plugin. In order to quantify cell types, 10-15 images were taken from the dorsal medial, dorsal lateral, ventral medial, and ventral lateral regions, across 3-4 sections of the OE. Cell counts were averaged and converted to number of cells/mm of OE.

### **3.6 Acknowledgments**

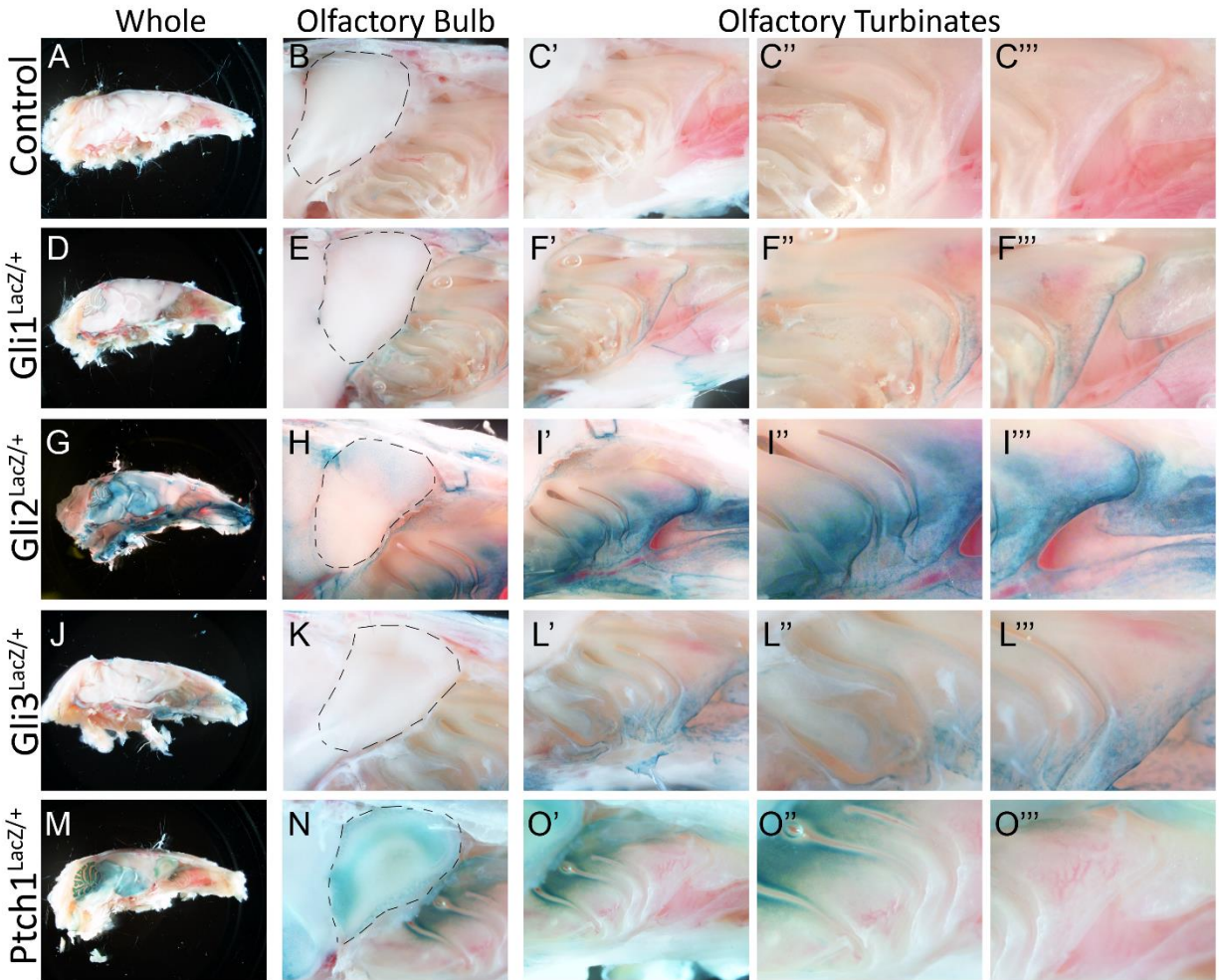
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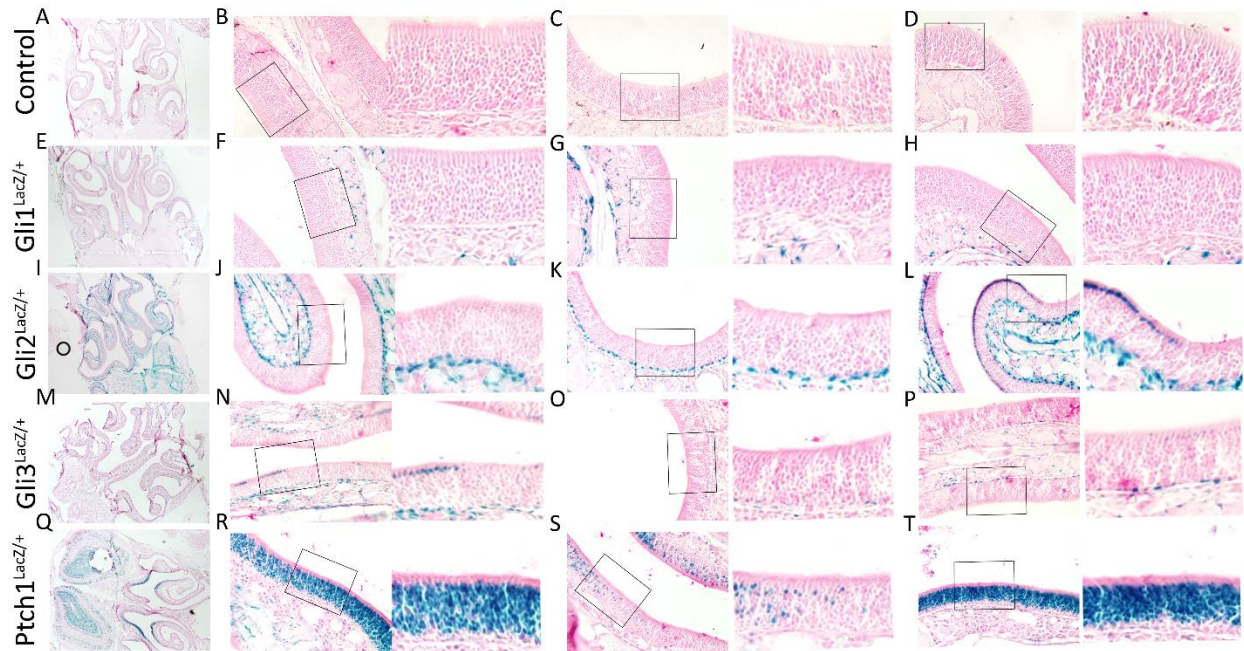
### 3-7 Figures



**Figure 3-1. GLI2 processing and corresponding genotypes.** Schematic illustration of GLI2 constructs used in transgenic mouse models. **A**, GLI2 has a DNA-binding domain and C-terminal activation domain, causing it to be a weak activator of the HH pathway in the presence of HH ligand. **B**, In the Gli2ΔN construct, when the N-terminal repressor domain is removed, GLI2 can act as a constitutive activator of the HH pathway independent of HH ligand. **C**, When the C-terminal activator domain of GLI2 undergoes proteolytic cleavage, it like GLI3, acts as a repressor in the absence of HH ligand. **D**, In the Gli2ΔC4 construct, when the C-terminal activator domain is removed, GLI2 acts as a constitutive repressor of the HH pathway independent of HH ligand.

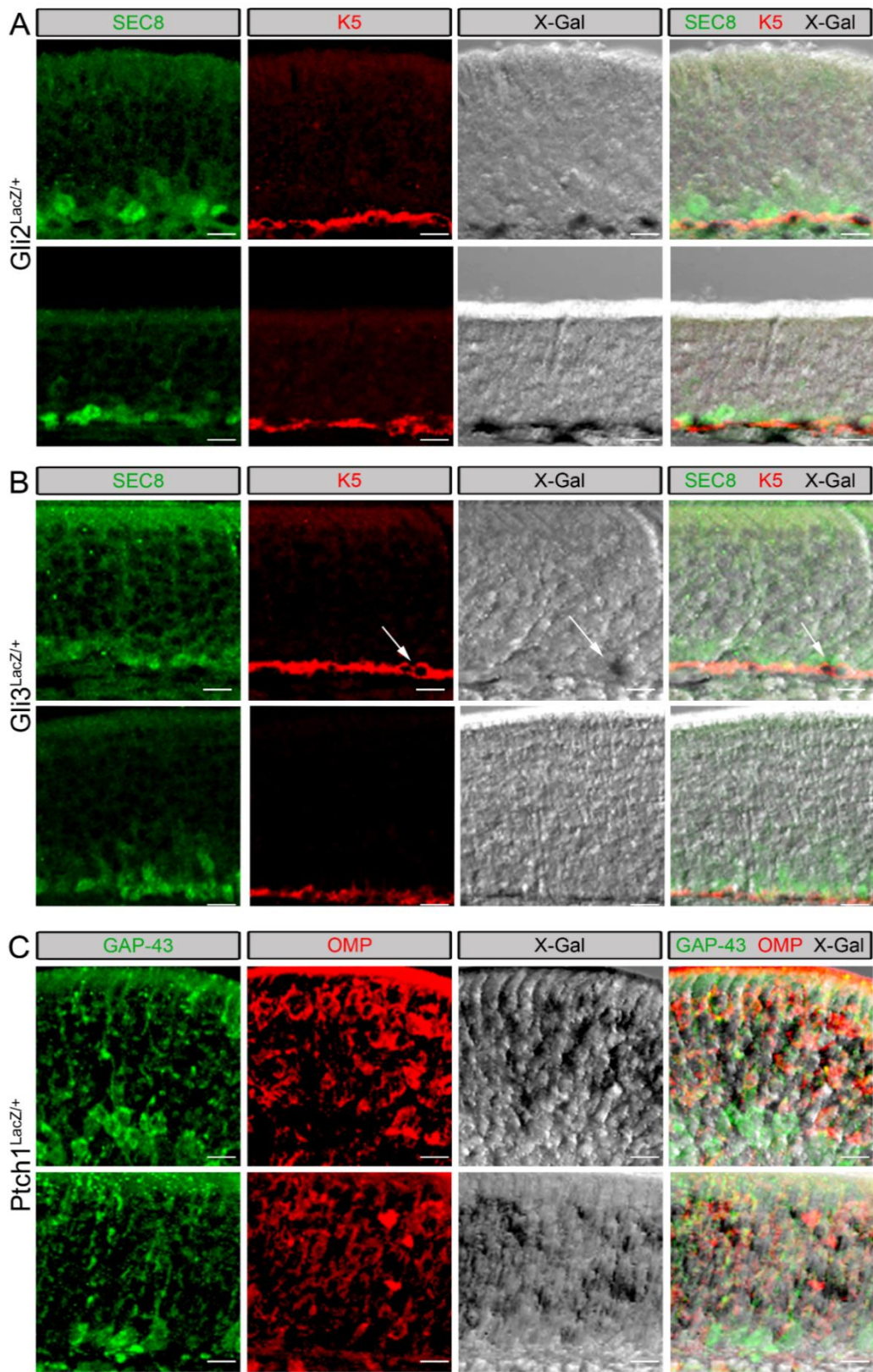


**Figure 3-2. Components of the HH pathway are present in the CNS and olfactory turbinates.** Whole heads of Control, *Gli1<sup>lacZ/+</sup>*, *Gli2<sup>lacZ/+</sup>*, *Gli3<sup>lacZ/+</sup>*, and *Ptch1<sup>lacZ/+</sup>* mice were incubated with an X-Gal substrate that is cleaved by  $\beta$ -Galactosidase, producing a blue precipitate that indicates *lacZ* expression. (A-C''') Control mice show no color. (E) *Gli1* is not expressed in the olfactory bulb (OB) but (F'-F''') in the stoma of olfactory turbinates. (H) *Gli2* is expressed in the dorsal OB and (I'-I''') anterior/ventral parts of the olfactory turbinates. (J) *Gli3* is not expressed in the OB but (L'-L''') similar to *Gli2*, is expressed in anterior/ventral parts of the olfactory turbinates at a lesser intensity. (N) *Ptch1* is expressed in the entire OB and (O'-O''') in an opposing gradient to *Gli2* and *Gli3* in posterior/dorsal parts of the olfactory turbinates.



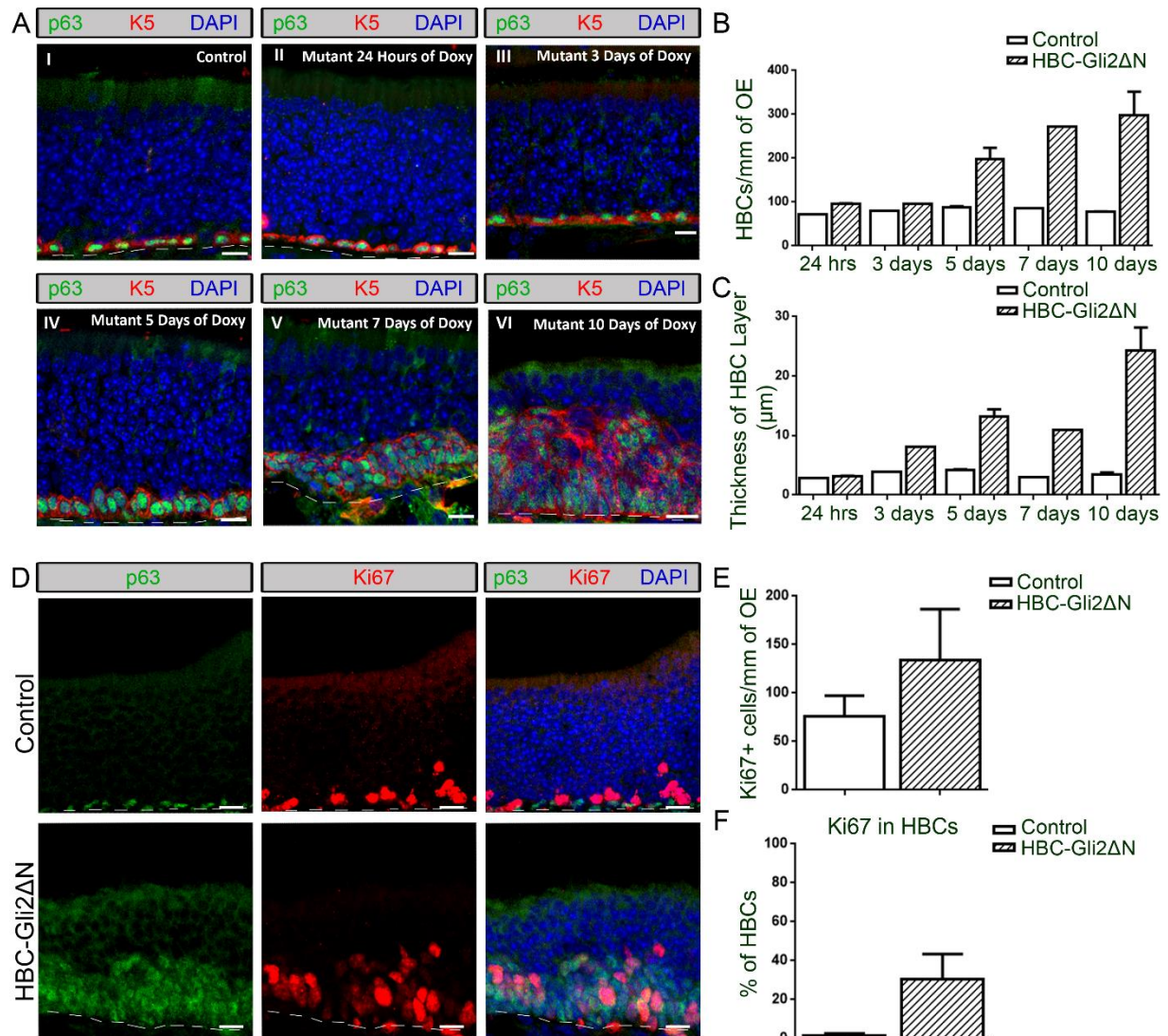
**Figure 3-3. Components of the HH pathway are present in specific cells of the OE.** Tissue sections from Control, *Gli1<sup>lacZ/+</sup>*, *Gli2<sup>lacZ/+</sup>*, *Gli3<sup>lacZ/+</sup>*, and *Ptch1<sup>lacZ/+</sup>* mice were incubated with an X-Gal substrate that is cleaved by  $\beta$ -Galactosidase, producing a blue precipitate that indicates *lacZ* expression. (A-D) Control mice show no color in the OE or lamina propria (LP). (E-H) *Gli1* is not expressed in the OE, but in cells of the LP. (I-L) *Gli2* is uniformly expressed in basally located cells in the OE, a majority of cells in the LP, and a subset of SUS cells in the apical OE. (M-P) *Gli3* is sparsely expressed in basally located cells of the OE and cells in the LP, and also a subset of SUS cells. (Q-T) *Ptch1* is expressed with high intensity in a majority of more apically located cells, but not SUS cells, and with lower intensity in basally located cells. The expression pattern is “patchy.”



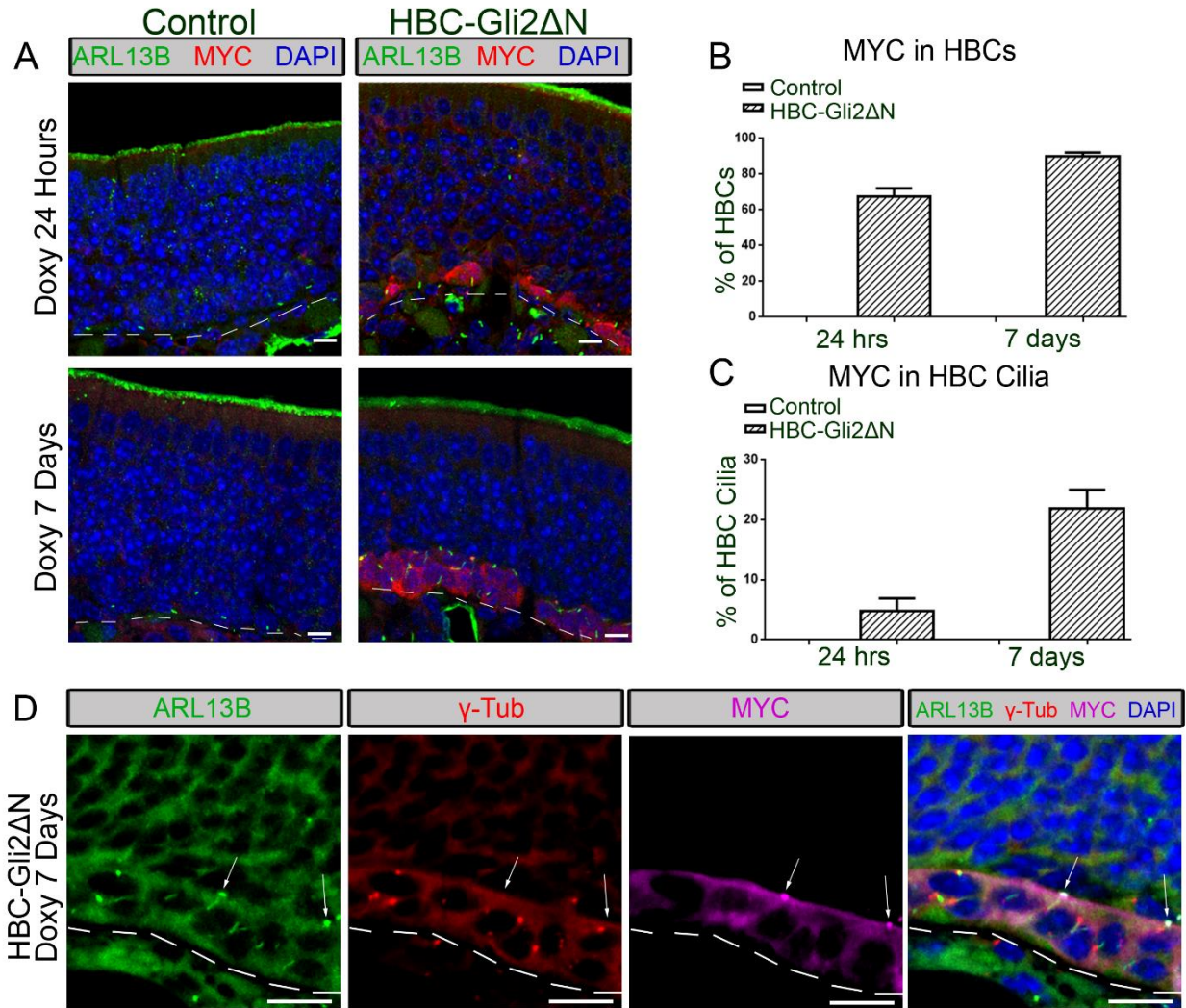




**Figure 3-4. The HH transcription factors *Gli2* and *Gli3* are expressed specifically in HBCs of the OE, while *Ptch1* is expressed in mature OSNs.** Dual X-gal and immunofluorescence staining of coronal sections of the OE in *lacZ* reporter mice. (A) *Gli2* is expressed in all K5+ HBCs but not in SEC8+ GBCs. (B) *Gli3* is expressed in fewer K5+ cells (arrow) but also excluded from SEC8+ GBCs. (C) *Ptch1* is specifically expressed in a subset of mature OSNs.

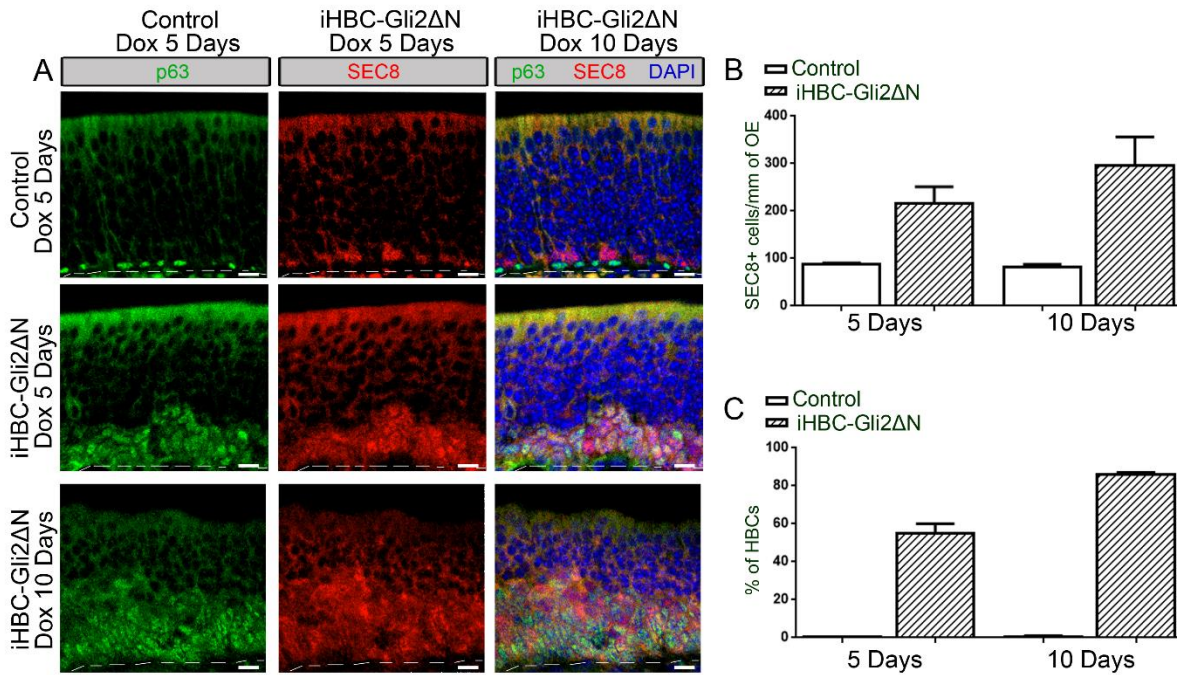


**Figure 3-5. Constitutively active *Gli2* in HBCs results in hyperproliferation.** (A) Immunofluorescence analysis of p63<sup>+</sup>/K5<sup>+</sup> HBCs in the OE of (I) control mice and iHBC-Gli2ΔN mice treated with doxy for (II) 24 hours, (III) 3 days, (IV) 5 days, (V) 7 days, or (VI) 10 days. (B) Quantified data show an increase in the number of HBCs in iHBC-Gli2ΔN mice treated with doxy for at least 5 or more days compared to control mice. (C) Quantified data reveal that the thickness of the HBC layer subsequently increases in iHBC-Gli2ΔN mice compared to control mice. (D) While control mice possess p63<sup>+</sup> HBCs devoid of Ki67, iHBC-Gli2ΔN mice treated with doxy for 10 days, show an increase in the number of Ki67<sup>+</sup> cells and Ki67 expression in p63<sup>+</sup> HBCs. (E) Quantified data show an overall increase in the number of Ki67<sup>+</sup> cells in the OE of iHBC-Gli2ΔN mice compared to control mice. (F) Quantified data show that in iHBC-Gli2ΔN mice, nearly 40% of p63<sup>+</sup> HBCs are also Ki67<sup>+</sup>, while no HBCs express Ki67 in control mice.

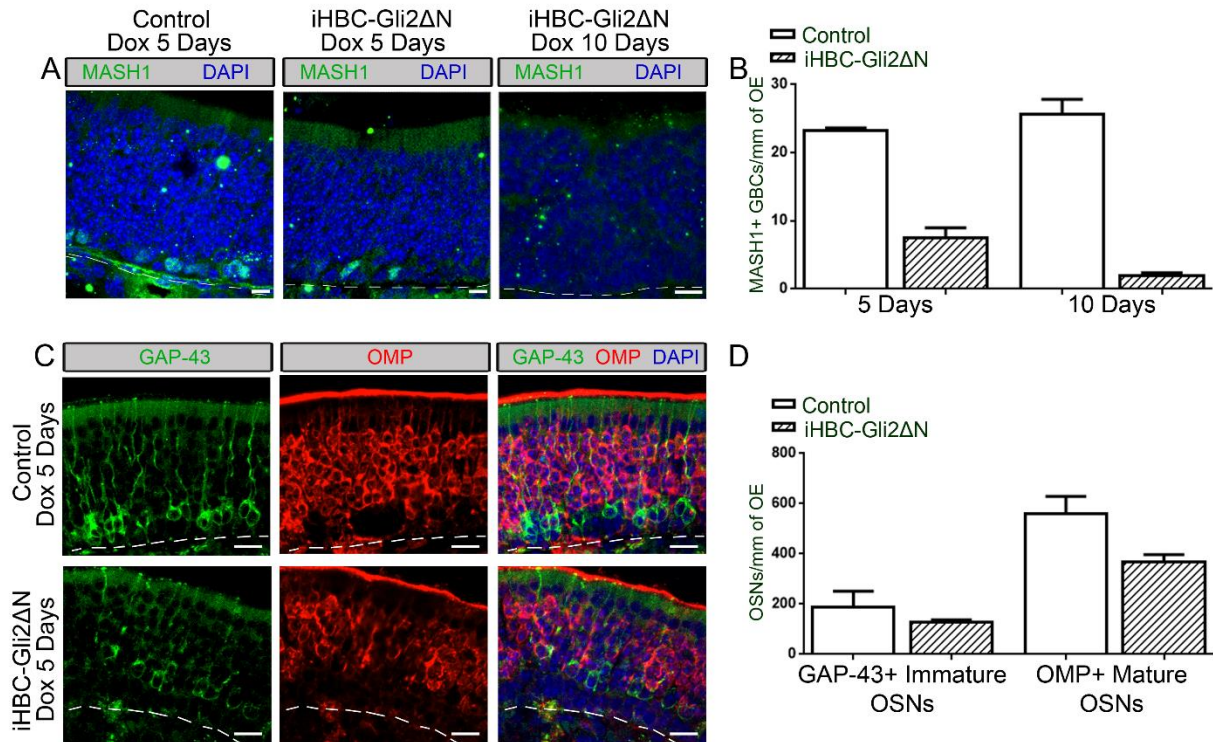


**Figure 3-6. GLI2 localizes to tips of HBC cilia.** IF analysis of control and iHBC-Gli2ΔN mice reveals (A) expression of MYC in HBCs (indicative of ARL13B+ cells) of iHBC-Gli2ΔN mice after 24 hours or 7 days of dox, which is absent in control mice. (B) Quantified data show that compared to controls, 60% of HBCs express MYC in iHBC-Gli2ΔN mice treated with dox for 24 hours which increases to 90% of HBCs after 7 days. (C) Quantified data show that control mice do not have MYC expression in ARL13B+ HBC cilia, while iHBC-Gli2ΔN mice treated with dox for 24 hours exhibit MYC in ~10% of HBC cilia and those treated for 7 days exhibit MYC in ~25% of HBC cilia. (D) IF analysis shows MYC-labeled GLI2 localizes to tips of ARL13B+ cilia in opposition of γ-tubulin+ basal bodies in MYC-labeled HBCs of iHBC-Gli2ΔN mice treated with dox for 7 days.

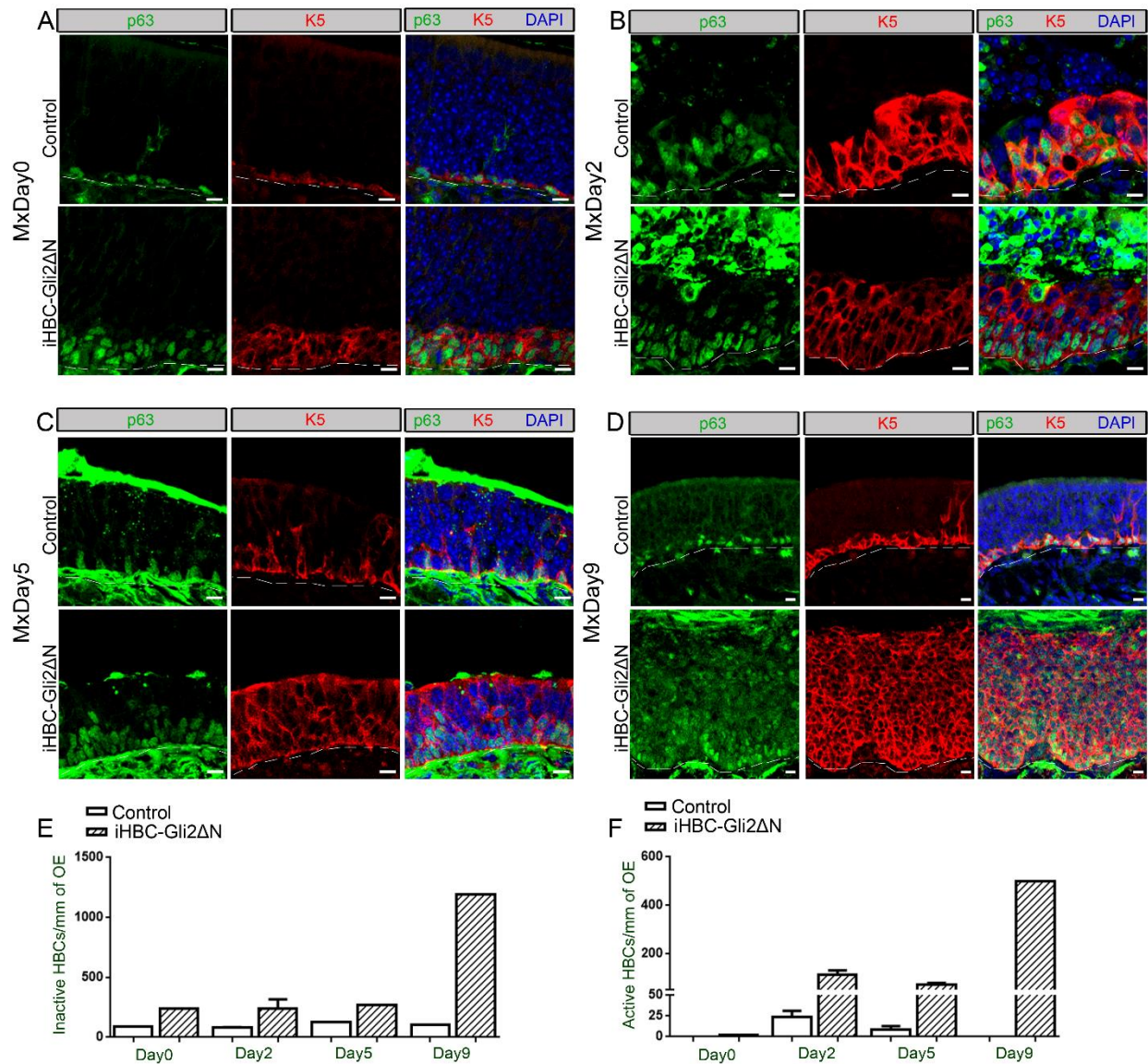




**Figure 3-7. Constitutively active *Gli2* in HBCs results in the upregulation of SEC8.** IF analysis of control and iHBC-Gli2ΔN mice reveals (A) an upregulation of SEC8 in HBCs of iHBC-Gli2ΔN mice represented by the co-expression of SEC8 in p63+ HBCs treated with dox for 5 or 10 days. (B) Quantified data show the total number of SEC8+ cells in the OE of iHBC-Gli2ΔN mice treated with dox for 5 or 10 days is increased compared to control mice. (C) Quantified data show that while the percentage of HBCs in control mice have no SEC8 expression, 60% of HBCs in iHBC-Gli2ΔN mice treated with dox for 5 days and 90% of HBCs in iHBC-Gli2ΔN mice treated with dox for 10 days have SEC8 expression.



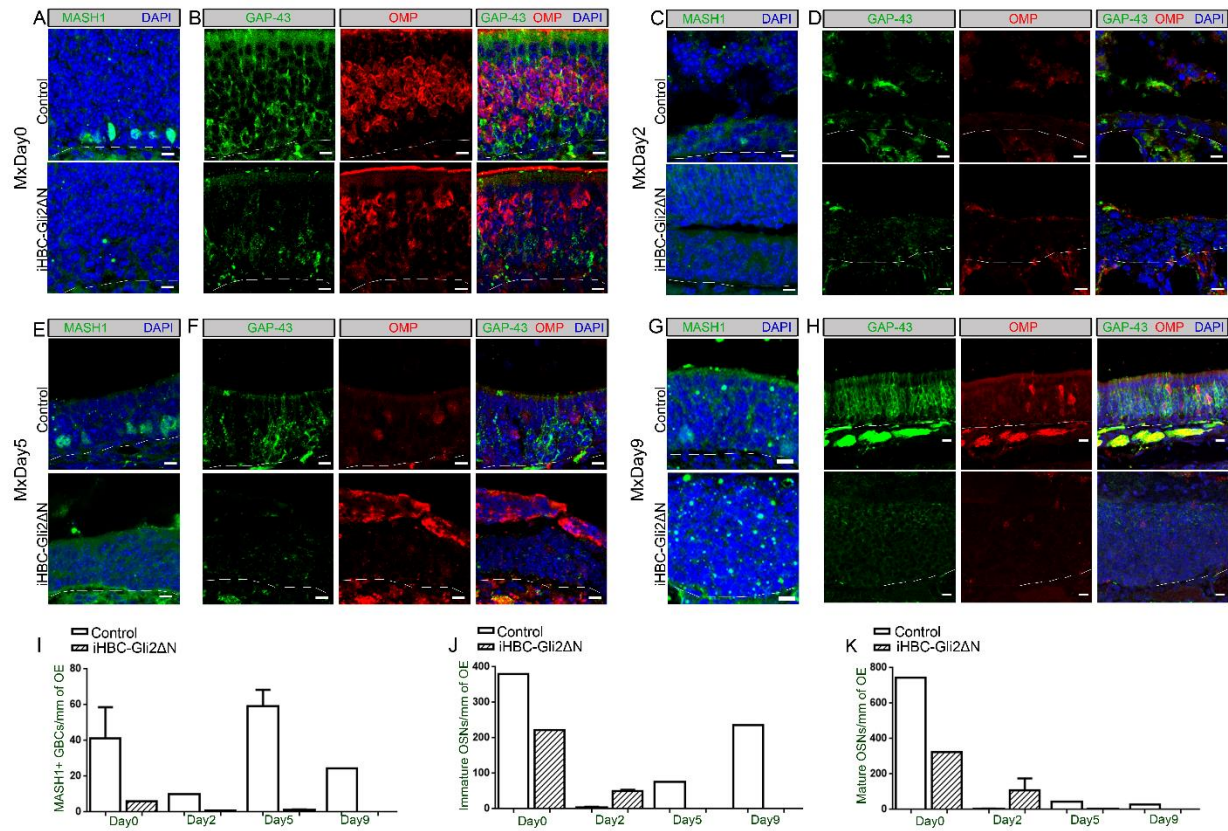
**Figure 3-8. Constitutively active *Gli2* in HBCs results in the loss of neuronal cells.** (A) IF analysis of control and iHBC-Gli2ΔN mice and (B) quantified data reveal a dramatic reduction in the number of MASH1+ GBCs in iHBC-Gli2ΔN mice treated with dox for 5 or 10 days compared to control mice. (C) IF analysis and (D) quantified data show a loss of GAP-43+ immature and OMP+ mature OSNs in iHBC-Gli2ΔN mice treated with dox for 5 days compared to controls.



**Figure 3-9. Constitutively active *Gli2* in HBCs results in an increase in the number of active and inactive HBCs during the regeneration of the OE.** Control and iHBC-Gli2ΔN mice were treated with dox for 5 days and administered an I.P. injection of MMI to induce injury to the OE. IF analysis of p63+/K5+ inactive HBCs and p63-/K5+ active HBCs reveals that (A) at Day 0 of injury, there is an increase in the number of p63+/K5+ inactive HBCs of iHBC-Gli2ΔN mice, which (B) by 2 days following injury, increases in both control and iHBC-Gli2ΔN mice with additional p63-/K5+ active HBCs present. (C) After 5 days of recovery, HBCs of control mice appear to return to an inactive state while iHBC-Gli2ΔN mice continue to possess an increased number of p63+/K5+ inactive and p63-/K5+ active HBCs. (D) At 9 days following injury, HBCs of control mice are similar to Day 0, but the number of p63+/K5+ inactive and p63-/K5+ active HBCs continue to dramatically increase in number. Quantified data of (E) inactive HBCs and (F) active

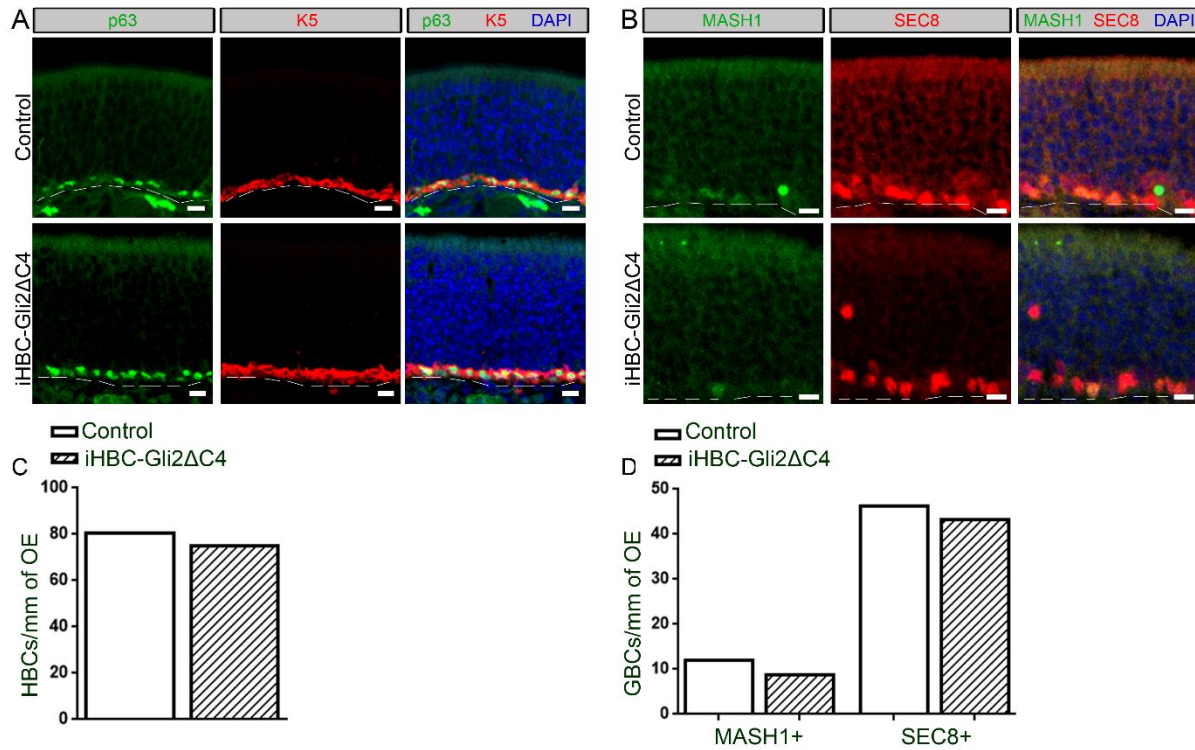
HBCs reveal that HBCs of both control and iHBC-Gli2 $\Delta$ N mice become active but while HBCs of control mice eventually become inactive, HBCs of iHBC-Gli2 $\Delta$ N mice continue to be active.



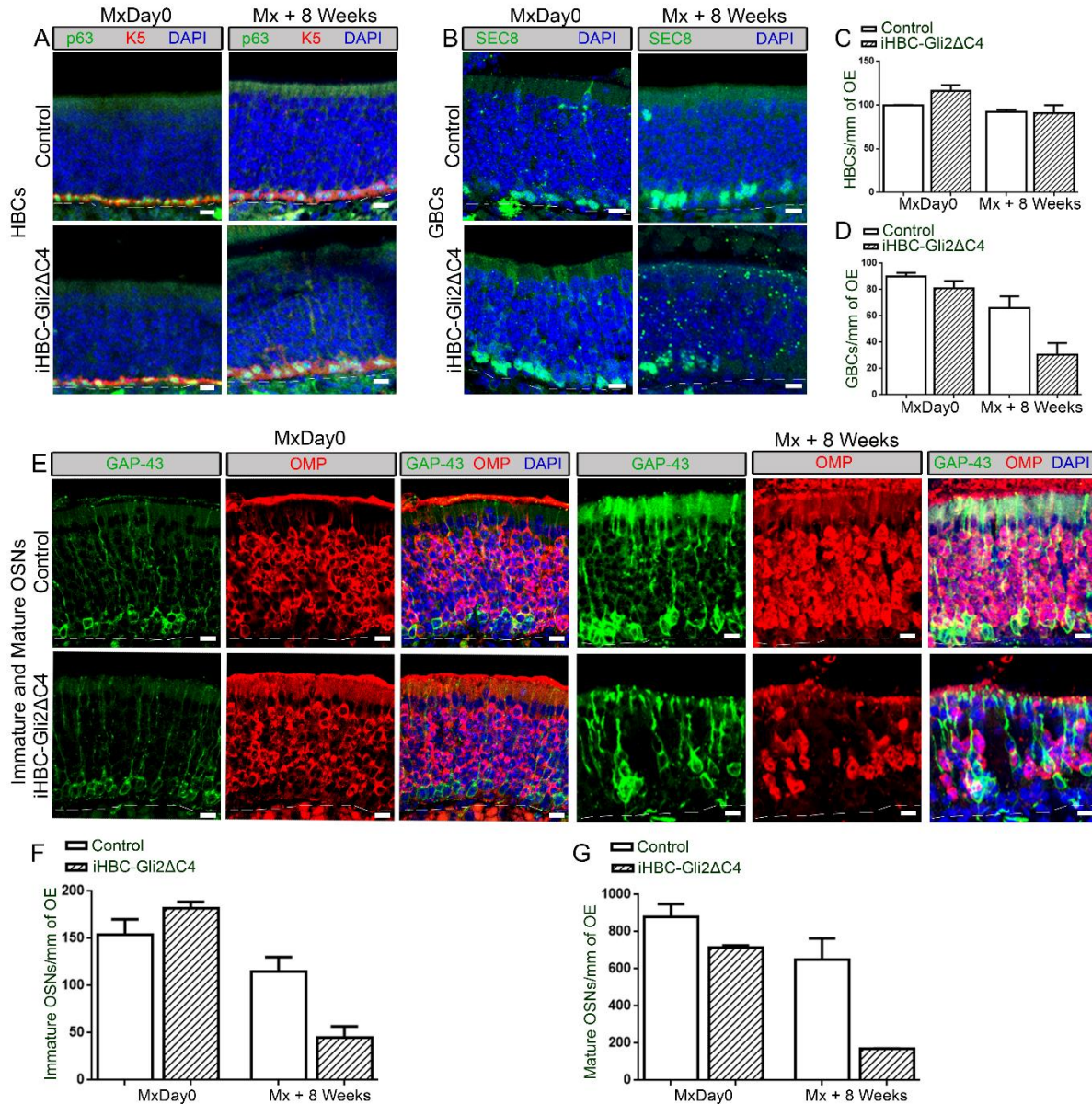


**Figure 3-10. Constitutively active *Gli2* in HBCs results in the loss of neurogenesis during the regeneration of the OE.** Control and iHBC-Gli2ΔN mice were treated with dox for 5 days and administered an I.P. injection of MMI to induce injury to the OE. IF analysis reveals that at Day 0 of injury, there is a reduction in the number of (A) MASH1+ GBCs and (B) GAP-43 immature and OMP+ OSNs in iHBC-Gli2ΔN mice compared to control mice. By 2 days following injury, there is a decrease in (C) MASH1+ GBCs and (D) GAP-43 immature and OMP+ OSNs in both control and iHBC-Gli2ΔN mice. Following 5 days of recovery, (E) MASH1+ GBCs and (F) GAP-43 immature and OMP+ OSNs return in control mice, but are still absent in iHBC-Gli2ΔN mice. At 9 days following injury, (G) MASH1+ GBCs are still present in control mice but absent in iHBC-Gli2ΔN mice, while (H) there is a further return of GAP-43 immature and OMP+ OSNs in control mice but no OSNs present in iHBC-Gli2ΔN mice. Quantified data of (I) MASH1+ GBCs, (J) immature OSN, and (J) mature OSNs show a marked decrease in neuronal cells of control and iHBC-Gli2ΔN mice following MMI-induced injury that return in control mice but not in iHBC-Gli2ΔN mice.



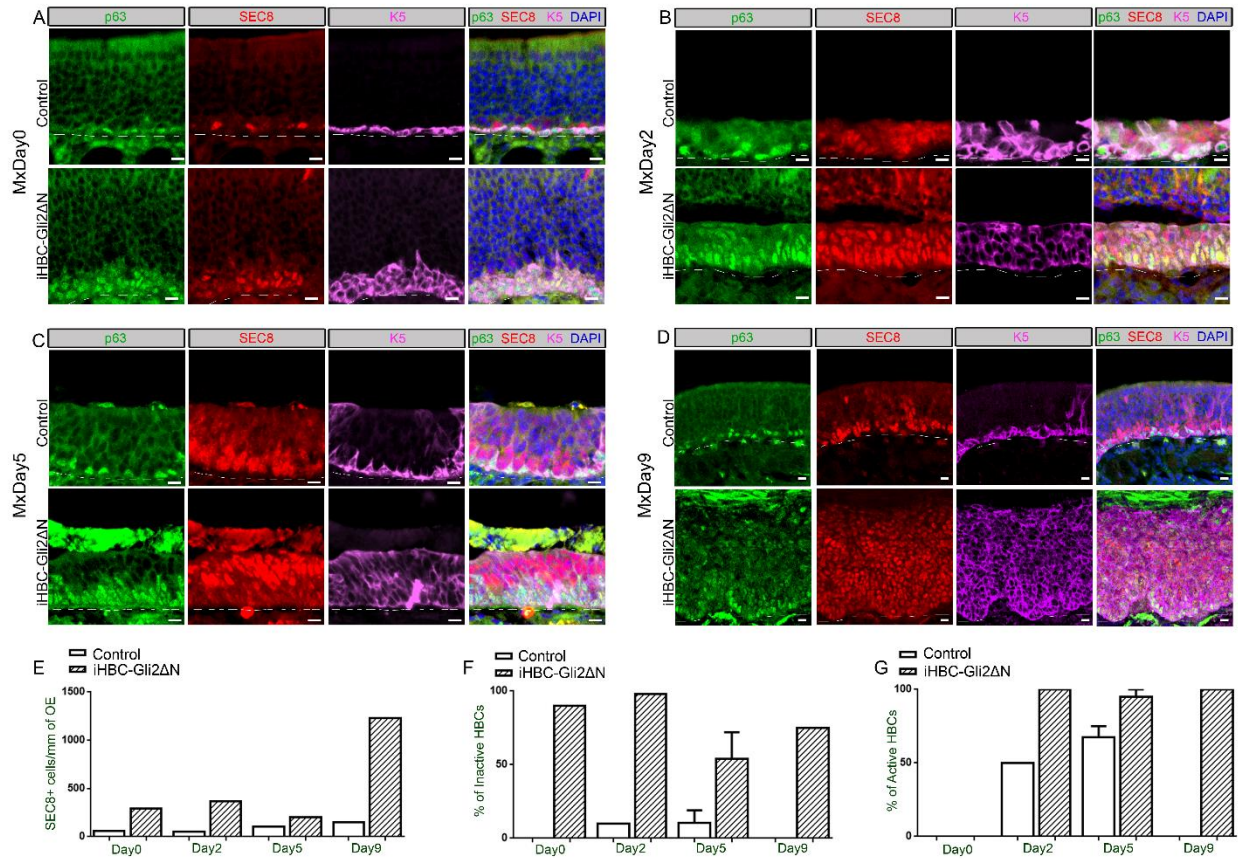


**Figure 3-11. Dominant negative repressive *Gli2* in HBCs has no effect on homeostasis of the OE.** Following 36 days of dox treatment, (A-B) IF analysis of control and iHBC-Gli2ΔC4 mice and (C-D) quantified data reveal no difference in the number of (A, C) p63+/K5+ HBCs or (B, D) MASH1+ and SEC8+ GBCs.

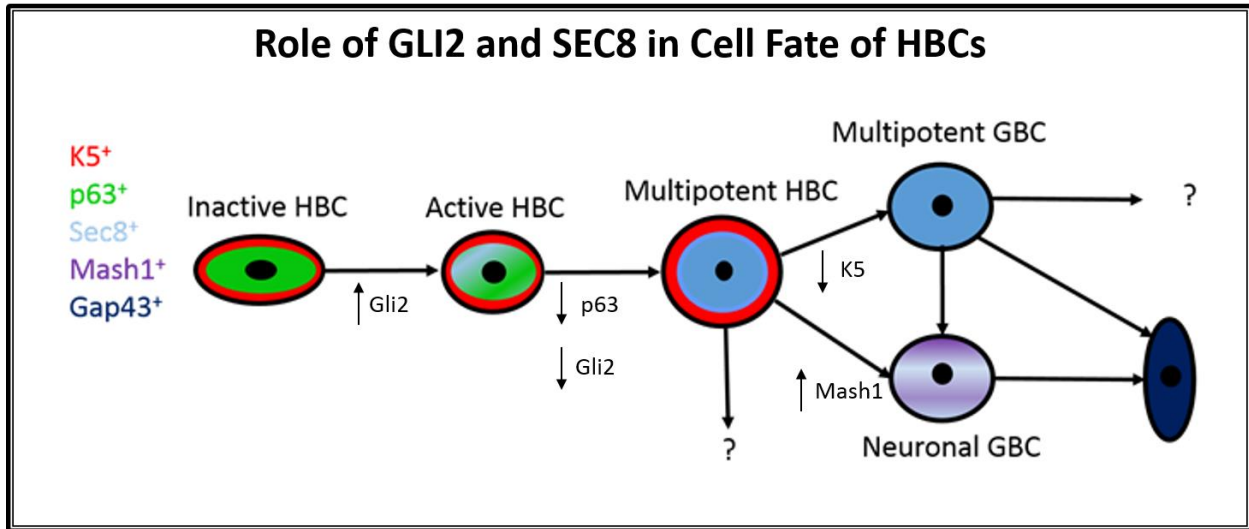


**Figure 3-12. Dominant negative repressive *Gli2* in HBCs results in the improper regeneration of the OE.** Control and iHBC-Gli2ΔC4 mice were treated with dox for 7 days and administered an I.P. injection of MMI to induce injury to the OE. (A) IF analysis and (C) quantified data reveal that the number of p63+/K5+ HBCs at Day 0 of injury and following 8 weeks is similar between control and iHBC-Gli2ΔC4 mice. (B) IF analysis and (D) quantified data show no difference in the number of SEC8+ GBCs at Day 0 between control and iHBC-Gli2ΔC4 mice but a decrease in GBCs of iHBC-Gli2ΔC4 mice 8 weeks following injury. The number of (E, F) GAP-43 immature and (E, G) OMP+ mature OSNs is unchanged in iHBC-Gli2ΔC4 mice compared to control mice at Day 0 of injury but following 8 weeks of recovery, there is a dramatic decrease in the number of OSNs in iHBC-Gli2ΔC4 mice compared to control mice.





**Figure 3-13. Constitutively active *Gli2* in HBCs impedes the differentiation of HBCs during regeneration of the OE.** Control and iHBC-Gli2ΔN mice were treated with dox for 5 days and administered an I.P. injection of MMI to induce injury to the OE. (A) At Day 0 of the injury, there is an upregulation of SEC8 in p63+/K5+ inactive HBCs of iHBC-Gli2ΔN mice while control mice possess SEC8+ GBCs that are not co-expressed with K5 or p63. (B) After 2 days of recovery, control mice exhibit some upregulation of SEC8 in p63+/K5+ inactive HBCs and p63-/K5+ active HBCs which is consistently seen in both groups of HBCs in iHBC-Gli2ΔN mice. (C) At 5 days following injury, control mice show a normal appearance of p63+/K5+ inactive HBCs and SEC8+ GBCs while iHBC-Gli2ΔN mice continue to show an upregulation of SEC8 in p63+/K5+ inactive and p63-/K5+ active HBCs. (D) By 9 days of recovery, control mice exhibit normal HBC and GBC expression profiles, while iHBC-Gli2ΔN mice continue to show an increased number of p63+/K5+ inactive and p63-/K5+ active HBCs that co-express SEC8. Quantified data reveal that (E) the total number of SEC8+ cells is dramatically increased in iHBC-Gli2ΔN mice before and following injury compared to control mice, (F) the percentage of inactive HBCs that co-express SEC8 is largely in iHBC-Gli2ΔN mice regardless of injury and (G) a large percentage of active HBCs co-express SEC8 following injury in both control and iHBC-Gli2ΔN mice but only in iHBC-Gli2ΔN mice do active HBCs still express SEC8 9 days following injury.



**Figure 3-14. Model of GLI2- and SEC8-dependent transition of HBCs to GBCs during neurogenesis in the OE.** Normally GLI2 acts as a repressor to maintain HBC quiescence (p63<sup>+</sup>/K5<sup>+</sup>). Upon injury, HBCs are activated and GLI2 acts as an activator which upregulates Sec8 (p63<sup>+</sup>/K5<sup>+</sup>/SEC8<sup>+</sup>). In order for HBCs to become multipotent (K5<sup>+</sup>/Sec8<sup>+</sup>) and contribute to differentiation and regeneration in the OE, p63 must be downregulated which should lead to downregulation of *Gli2*, and subsequent differentiation. However, because the constitutive form of *Gli2* is driven by the *K5* promoter which I propose to be expressed in multipotent cells, HBCs are fixed in an active and multipotent state and unable to differentiate into neuronal cells to replenish the OE.

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## **Chapter IV:**

### **Discussion and Future Directions**

#### **4.1 A Novel Role for Primary Cilia in the Regulation of Olfactory Horizontal Basal Cells and Neurogenesis**

##### 4.1.1 Summary of Key Findings

Data presented in Chapter II demonstrate a novel role for primary cilia in olfactory neurogenesis. I provide evidence that horizontal basal cells (HBCs) in the olfactory epithelium (OE) selectively possess primary cilia. My data support the paradigm that primary cilia are essential regulators of adult tissue homeostasis and neurogenesis (Han et al., 2008; Tummala et al., 2010; Amador-Arjona et al., 2011; Croyle et al., 2011; Kumamoto et al., 2012). Adult stem cells, like HBCs, often remain quiescent in adult tissues unless activated by an injury from which they generate multiple cell types (Veland et al., 2009). Primary cilia are often associated with the G0 stage or quiescent phase of the cell cycle (Plotnikova et al., 2009; Irigoien and Badano, 2011; Kim and Tsiokas, 2011). However, the adult stem cells that exist in a quiescent state make cell cycle considerations secondary to the need to respond to transient environment signals sensed through the cilia (Plotnikova et al., 2009). HBCs appear to work in this fashion – that is, primary cilia are not essential for control of the cell cycle (e.g. proliferation), but are important for sensing external signals that lead to their activation and differentiation. This observation is contrary to what is seen in other epithelia, such as the skin

(Croyle et al., 2011) but is similar to observations in neural stem cells (NSCs) of the SVZ where the loss of cilia also does not change the number of stem cells (Amador-Arjona et al., 2011). These data suggest a tissue-specific role for primary cilia in adult neurogenesis.

I also show that a loss of HBC cilia in iHBC-IFT88 null mice results in reduced neurogenesis during development. It is believed that GBCs and not HBCs contribute to developmental neurogenesis (Guillemot et al., 1993; Cau et al., 1997; Cau et al., 2002). This notion is strongly supported by the fact that HBCs appear late embryonically (Packard et al., 2011b). However, a recent study suggested that HBCs do contribute to neurogenesis during postnatal development (Iwai et al., 2008). My data support this recent finding of HBC-driven neurogenesis during early postnatal development. Interestingly, there are regional differences in this neurogenesis that could be attributed to the temporal and spatial release of morphogens during development (Vedin et al., 2009) or the regional differences of certain transcription factors expressed during development (Duggan et al., 2008).

Furthermore, I introduce SEC8 as a novel marker of GBCs. Several studies indicate that GBCs are neuronal precursors that exist as a heterogeneous population, compartmentalized by their expression of distinct transcription factors. In the GBC lineage cascade, *Ascl1* (*Mash1*) expression lies upstream of *Neurogenin1* (*Ngn1*) which lies upstream of, but also overlaps with, *NeuroD1* expression (Cau et al., 1997; Manglapus et al., 2004; Packard et al., 2011a; Krolewski et al., 2013). *NeuroD1* is eventually switched off prior to onset of post-mitotic differentiation, and low levels of *NeuroD1* are sometimes found in immature OSNs (Packard et al., 2011a). Recently, the chromatin modifying

protein LSD1, was shown to localize with ASCL1 (MASH1) expressing cells, a subgroup of NGN1 and SOX2 expressing cells, as well as a subpopulation of immature OSNs, (Krolewski et al., 2013). I show that SEC8 overlaps with all LSD1-expressing cells and a surplus of cells that are not HBCs or immature OSNs, suggesting that SEC8 labels a larger population of GBCs that span the entire lineage of cells. Interestingly, *Sec8* null embryos, similar to *Mash1* mutant mice, show a loss of *Notch1* (Friedrich et al., 1997; Cau et al., 2002), which is believed to be involved in GBC differentiation. These observations suggest that *Sec8* plays important roles in signaling in GBCs, perhaps through Notch signaling, that is necessary for their neuronal differentiation.

Due to their close association with other cell types in the OE and their expression of epidermal growth factor (EGF) receptor-like immunoreactivity, HBCs are primed to serve as a channel of communication to the GBCs about the status of the OE and other cell types (Carr and Farbman, 1992; Holbrook et al., 1995). My work supports the notion that HBCs and SUS cells make physical contact through HBC primary cilia that project into the interstitial space between SUS cell endfeet and HBCs (Joiner et al., 2015). These endfeet are proposed sites of communication (Jia and Hegg, 2010) and HBC primary cilia may act as a scaffold for this communication.

Overall, my studies support the idea that HBCs contribute to olfactory regeneration and introduce a new role for primary cilia in that regeneration. I also provide evidence of a role for HBCs in OE development that was thought to be limited to GBCs (Doty, 2003; Treloar et al., 2010), and introduce a new marker for GBCs that may be important for their differentiation. What remains unexplored are: 1) the specific mechanisms that primary cilia utilize to regulate HBC proliferation and cell fate determination, 2) a more complete

profile of HBC primary cilia during development, homeostasis, and regeneration, and 3) the identification of potential therapeutic approaches that target HBC primary cilia.

#### 4.1.2 Future Directions

##### *Are Primary Cilia Sensors of Injury that Also Dictate Cell Fate?*

It is possible that HBC primary cilia are both detectors of injury and signaling scaffolds for differentiation and cell fate determination. If HBC cilia are detectors of the insult, observing what happens to primary cilia immediately following injury upon activation of HBCs would be informative. Primary cilia could be reabsorbed prior to proliferation and re-established prior to differentiation or maintained throughout HBC activation and differentiation. Ciliary resorption is triggered by the addition of a specific combination of growth factors including PDGF $\alpha$  and either insulin-like growth factor1 (IGF-1), epidermal growth factor (EGF), or fibroblast growth factor (FGF) (reviewed in Kim and Tsiokas, 2011). These factors are positive regulators of neurogenesis in the OE and are most prominently expressed in HBCs and SUS cells (reviewed in Murdoch and Roskams, 2007). Analysis of these factors in the OE of iHBC-IFT88 null mice with and without an injury could provide insight to what possible signals HBCs detect following injury.

Upon cell death, SUS cells may release a signal to HBCs that is transduced through primary cilia, triggering HBC activation. Using an additional lesion model in which SUS cells are ablated, one could determine if there is a direct connection between SUS cell death and HBC activation. Ablation of the OE with NiSO<sub>4</sub> selectively causes SUS cell death with a subsequent increase in basal cell proliferation (Jia et al., 2010); however,

the population of basal cells was not defined. Analyzing the OE with specific HBC and GBC markers along with proliferative markers following a lesion with NiSO<sub>4</sub> in control and iHBC-IFT88 null mice could test the theory that SUS cell death activates HBCs and whether cilia are important for the detection of injury. Additionally, a specific ablation of SUS cells would provide more direct information about the relationship and communication between SUS cells and HBCs. There exists a transgene, *TetO-DTA* which leads to expression of diphtheria toxin A under control of a tetracycline operator (Lee et al., 1998). SUS cells express K18 specifically in the OE (Holbrook et al., 2011) and if expression of the tetracycline transactivator, rtTA, can be driven under the *K18* promoter (Ye et al., 2001), SUS cells could be specifically ablated to further analyze how HBCs respond. Ideally, this specific ablation of SUS cells should occur in iHBC-IFT88 null mice to determine if primary cilia are in fact necessary for detection of the insult but this breeding scheme would rely heavily on recombination and may not be possible.

Furthermore, cell-fate mapping with the use of either *K5-Cre-tdTomato* mice in which *K5* expressing cells and their progeny express tdTomato or inducible *K5-CreERT2-R26R* mice in which *K5* expressing cells and their progeny express *lacZ*. An inducible model would be ideal to investigate the lineage of HBCs following an injury in order to bypass any possible HBC-driven neurogenesis in development. Therefore *Ift88<sup>fl/fl</sup>* mice could be crossed with *K5-CreERT2-R26R* mice or the *K5rtTA;TetOCre;Ift88<sup>fl/fl</sup>* mice could be crossed with *R26R-tdTomato* mice to lineage trace HBCs in which cilia are ablated. The first cross would utilize a tamoxifen inducible system, while the second cross would utilize the doxycycline inducible system which I successfully utilized to remove cilia (see Chapter II). Both crosses would rely heavily on recombination and therefore, use of an

IFT88 null allele could alleviate some of this burden. Cell-fate mapping would ultimately elucidate what cells are derived from HBCs during regeneration of the OE and developmental neurogenesis. This technique would especially be important for circumventing the residual GBCs that remain after an MMI injury and incomplete loss of HBC cilia.

Interestingly, I noticed an increase in respiratory epithelia in iHBC-IFT88 null mice 8 weeks following MMI injury to the OE (Fig. 4-1). It is unknown whether this epithelia came from infiltration due to a loss of OSNs or from regeneration. Xie, et. al., showed through cell-fate mapping that respiratory regeneration comes from HBCs eight weeks following severe injury with the herbicide, dichlorobenzonitrile (DCBN) when there is a significant loss of GBCs (Xie et al., 2010). Most likely, multiple pathways and signaling factors work together to create the contribution of neurogenesis seen from HBCs. I speculate that during recovery, the first factor likely comes from the SUS cells alerting the HBCs to a severe lesion that requires the activation of both HBCs and GBCs. The second factor could come from GBCs, alerting the HBCs to take on a neuronal fate. Surprisingly, I saw no difference in cell death at 8 weeks post injury in iHBC-IFT88 null mice, but if there is more cell death in iHBC-IFT88 null mice earlier during recovery, this cell death might be necessary to trigger HBCs to regenerate tissue that, without a signal from GBCs, is fated to be respiratory. Analyzing the OE earlier during regeneration for apoptosis, respiratory markers, and using cell-fate mapping would elucidate whether the respiratory epithelia comes from HBCs or is a product of infiltration due to loss of OSNs. Additionally, SEC8 could be involved in communication with GBCs due to its role in exocytosis. Generating a conditional *Sec8* allele, *Sec8<sup>fl/fl</sup>*, and using the mouse line that expresses



CreER under the GBC promoter, *Ascl1* (*Mash1*), (*Ascl1*CreER) (Kim et al., 2011) could provide insight into this theory, although MASH1 is only present in a subset of GBCs.

#### *How do HBC Primary Cilia Change with Age and in Ciliopathy Models?*

As mentioned before, defects in primary cilia lead to various human diseases, termed ciliopathies, in which mutations of various genes that are involved in the formation and maintenance of primary cilia affect a variety of tissues and organ systems (Singla and Reiter, 2006; Hildebrandt et al., 2011). Ciliary defects also affect the OE, resulting in anosmia, a loss of smell (Kulaga et al., 2004; Tadenev et al., 2011; McIntyre et al., 2012). My identification of primary cilia on HBCs and their importance in neurogenesis reveal new mechanisms for the etiology of olfactory dysfunction. There are numerous reported etiologies for olfactory disturbance including environmental toxins and head injuries. In addition, the normal decline in olfactory function due to aging afflicts approximately 25% of the population over 65 years old and this estimation is thought to be largely underrepresented (Murphy et al., 2002). Although the olfactory basal cells are responsible for the regeneration and restoration of cells in the OE, there is a net loss of neurons over time due to the fact that the capacity to match OSN death with regeneration is compromised as a function of age (Conley et al., 2003). This compromise can be attributed to the dramatic decrease in basal stem cell proliferation with age, with olfactory cell proliferation decreasing ~10 to 15 times after birth during the first 3 months of life (Legrier et al., 2001; Ducray et al., 2002). Similarly, there is an age-related decline in the neurogenesis of the SVZ and the hippocampus (reviewed in Riddle and Lichtenwalner, 2007). Cilia may be associated with this loss of stem cell activation that seems to be a result of specific signals from the OE. If HBC cilia are depleted or become defective with

age, HBCs may become permanently inactive resulting in the inability to recover from an insult to the OE which would lead to a permanent loss of smell. Future work investigating age-related cilia loss or defects could define a mechanism for age-related anosmia. Additionally, analysis in the OE of ciliopathy mouse models in which the OE is ablated to determine if regeneration occurs normally could also translate to human ciliopathies in which HBC cilia may be affected (Kulaga et al., 2004; McIntyre et al., 2012).

#### *Potential Therapeutic Strategies for Olfactory Dysfunction.*

With their ability to generate multiple cell types, stem cells are potential therapeutic tools for tissue repair in various diseases including genetic and degenerative diseases as well as aggressive and recurrent cancers (Mimeault et al., 2007). However, stimulating their expansion and differentiation into functional progenitors remains a challenge due to the unknown drivers of differentiation. Olfactory basal stem cells can be cultured into neurospheres and transplanted back into mice in order to repopulate the OE (Jang et al., 2008; Krolewski et al., 2011). Additionally, adenoviral delivery of *Ift88* to mature OSNs in an *Ift88* deficient mouse model that exhibited loss of OSN cilia and resulting anosmia, restored cilia and olfactory function to mice (McIntyre et al., 2012). My preliminary data indicate that combining ablation of the OE via MMI treatment with adenoviral infection results in ectopic gene expression in HBCs (Fig. 4-2). Together, these studies provide a possible therapeutic strategy for olfactory loss that focuses on cilia function and its regulation of olfactory stem cell function. Future work could include analysis of cultured HBCs to study what happens with a loss of ciliary genes via siRNA, subsequent viral infection to rescue defects, and transplantation back into the OE. Additionally, iHBC-IFT88 null mice could be infected with adenovirus containing *Ift88* (McIntyre et al., 2012)

to determine if there is a genetic rescue of cilia and phenotypic rescue of regeneration and olfaction.

## 4.2 GLI-Dependent Role for Hedgehog Signaling in the Olfactory Epithelium

### 4.2.1 Summary of Key Findings

Data presented in Chapter III demonstrate a potential role for Hedgehog (HH) signaling in the olfactory epithelium (OE). Various HH components were found in specific cell types of the OE. Interestingly, their expression profiles differ from what is typical, specifically that *Ptch1* and *Gli1*, both of which are direct HH transcriptional targets, display distinct expression patterns. The HH transcription factors *Gli2* and *Gli3* were expressed selectively in HBCs but also in a subset of SUS cells. *Ptch1* appears to be present in a specific set of mature OSNs and at a lower levels in immature OSNs and some basal cells. I show that constitutive activation of *Gli2* in HBCs of iHBC-Gli2 $\Delta$ N mice results in their hyperproliferation with a resulting loss of neuronal cells. Although during normal homeostasis constitutive *Gli2* has dramatic effects on the composition of the OE, expression of a dominant negative *Gli2* repressor in iHBC-Gli2 $\Delta$ C4 mice has no effect. These data suggest that GLI2 acts as a transcriptional repressor in the OE. Although GLI2 is typically processed as an activator (Pan et al., 2006), studies have shown GLI2 can act as a repressor (Buttitta et al., 2003). Additionally, I demonstrate that both the activator and repressor forms of GLI2 lead to impaired regeneration following injury in the OE. These data suggest that GLI2 must be properly regulated in order for HBCs to contribute

to regeneration. Overall, these data implicate HH signaling, specifically *Gli2*, in the regulation of HBCs and their contribution to neurogenesis in the OE.

Furthermore, I show an upregulation of the GBC marker, SEC8, in HBCs of iHBC-*Gli2* $\Delta$ N mice, but this observation is not seen when HBCs express the repressive form of *Gli2* in *Gli2* $\Delta$ C4 mice. The SEC8<sup>+</sup> HBCs remain in the regenerating OE following injury and appear to be unable to transition to GBCs and eventually differentiate into OSNs. These data suggest that GLI2 and SEC8 are important for regulating HBC transition from dormancy to activation and ultimately differentiation into GBCs. Reports show that *Gli2* is a direct transcriptional target of p63 (Ram Kumar et al., 2014) and that downregulation of p63 in response to injury and subsequent activation could downregulate *Gli2*, driving HBC differentiation. What remains unexplored is: 1) the role *Gli3* plays in regulation of HBCs, 2) whether there are any redundancies between *Gli2* and *Gli3*, 3) a possible non-canonical role for HH signaling in different aspects of olfactory tissue homeostasis, and 4) the link between HBC primary cilia and HH signaling.

#### 4.2.2 Future Directions

##### *GLI Processing in the OE and Possible Redundant Roles*

I show that *Gli2* and *Gli3* transcripts are present in HBCs but what remains unknown is how the resulting proteins are processed. It is possible that GLI2 acts as a repressor in HBCs. Normally, HBCs are quiescent but when the constitutively active form of GLI2 is expressed, HBCs become proliferative. If GLI2 was normally processed as a weak activator (Sasaki et al., 1999), it would seem plausible for HBCs to be more proliferative and not quiescent. Because *Gli2* transcript is present in HBCs, it is likely that

GLI2 protein is either targeted for degradation or processed into a repressor. Furthermore, preliminary data show that staining the OE of control mice, iHBC-Gli2 $\Delta$ N mice, or HBC-Gli2 $\Delta$ C4 mice with an antibody against GLI2 that detects the C terminus, but not the N terminus (Cho et al., 2008), is seen in HBCs of HBC-Gli2 $\Delta$ N mice but not control or HBC-Gli2 $\Delta$ C4 mice (Fig. 4-3). These data further suggest that GLI2 is processed into an N-terminal repressor since the antibody can only detect residues near the C terminus. Additional analysis to detect protein levels of full length GLI2 and GLI3, as well as repressor and active forms would help elucidate the roles of these transcription factors. In order to detect the protein levels specifically in HBCs, cell sorting for Beta-Galactosidase in *Gli2*<sup>lacZ/+</sup> and *Gli3*<sup>lacZ/+</sup> mice could be utilized with Western blot analysis combined with qRT-PCR analysis to detect other HH components in HBCs.

My preliminary data indicate that in mice containing an HBC-specific deletion of *Gli2* (*K5-rtTA;TetO-Cre;Gli2*<sup>fl/fl</sup>), there is no change in OE cell composition during normal homeostasis and following an MMI-induced injury to the OE (Fig. 4-4). Unfortunately, because there are no commercially available antibodies to detect the active or repressor forms of GLI2 for immunohistochemistry, it is difficult to determine a loss of *Gli2* in the HBCs of these mice. In order to ensure that proper recombination occurs, *K5-rtTA;TetO-Cre;Gli2*<sup>fl/fl</sup> mice can be crossed with *Gli2*<sup>lacZ/+</sup> mice so that cell sorting for Beta-Galactosidase can be used to isolate HBCs and assess recombination efficiency via qRT-PCR. Western blot analysis of the entire OE of *K5-rtTA;TetO-Cre;Gli2*<sup>fl/fl</sup> lysates can also be used to verify a loss of GLI2 protein. If recombination and subsequent loss of *Gli2* successfully occurs and there is still no phenotype seen with a loss of *Gli2*, *Gli3* could play a redundant role in HH signaling since it is also expressed in HBCs.

In certain cases, including the development of the anterior neural tube (Motoyama et al., 2003), skeletal development (Mo et al., 1997), and development of the lung, trachea, and esophagus (Motoyama et al., 1998) *Gli2* and *Gli3* play redundant roles. However, this redundancy is unexplored in the adult. In order to elucidate the possible redundant role of *Gli2* and *Gli3* specifically in HBCs, a conditional knockout of *Gli3* can be utilized. The laboratory of Dr. Alex Joyner has already generated a *Gli3<sup>fl/fl</sup>* mouse (Blaess et al., 2008). Successful breeding of *K5-rtTA;tetO-Cre* mice with *Gli3<sup>fl/fl</sup>* mice will produce an inducible HBC-specific *Gli3* conditional null mouse (*K5-rtTA;tetO-Cre;Gli3<sup>fl/fl</sup>*). If no phenotype is seen in normal homeostasis or following an MMI-induced injury, mice with a conditional loss of both *Gli2* and *Gli3* (*K5-rtTA;tet-OCre;Gli2<sup>fl/fl</sup>;Gli3<sup>fl/fl</sup>*) could also be generated. Again, for analysis of loss of GLI2 and GLI3 proteins, *lacZ* can be introduced as one allele (for either *Gli2* or *Gli3*) and subsequent cell sorting can be performed. Additionally, cell-fate mapping with a tdTomato reporter can be used to determine what cells, if any, stem from HBCs that lack *Gli2*, *Gli3* or a combination of both following an injury and during normal tissue homeostasis.

#### *Non-Canonical Role of Hedgehog Signaling in the Olfactory Epithelium*

There are a few examples where a subset of the components of the canonical HH signaling pathway regulate various basic cellular processes seemingly independent of the full pathway. PTCH1 has been implicated in cell cycle regulation through interaction with cyclin B1 which acts at the G2/M checkpoint and is required for cell cycle progression (Barnes et al., 2001). Additionally, although not commonly described as non-canonical HH signaling, a role for the GLI transcription factors independent of the traditional HH ligand/SMO-signaling cascade has also been reported, particularly in cancer, where other

signaling pathways appear to directly regulate GLI proteins (reviewed in Stecca and Ruiz, 2010). RAS, MAPK, and PI3/AKT signaling have all been implicated in the modulation of GLI proteins as well as receptor tyrosine kinase (RTK) signaling (Aberger et al., 2012). The growth factors, EGFR, TGF $\beta$ , and IGF2 were also shown to be implicated in SMO-independent but GLI-dependent signaling (Aberger et al., 2012).

Although I have not examined the expression of *Smo*, it is believed to be expressed in the OE (Gong et al., 2009). Preliminary data from mice treated with the SMO antagonist, LDE-225 (Pan et al., 2010), a HH pathway inhibitor, showed no change in HBCs or the cell composition of the OE during natural turnover and in response to an MMI-induced lesion (Fig. 4-5), suggesting that the regulation of HBCs and OE regeneration is not HH ligand- or SMO-dependent. These findings were further supported by my data from mice containing an HBC-specific deletion of *Smo* (*K5-rtTA;TetO-Cre;Smo<sup>fl/fl</sup>*), in which there was no change in the cell composition of the OE during natural turnover (Fig. 4-6). *Smo* could still play a role upon injury to the OE, therefore, an MMI-induced injury in *K5-rtTA;TetO-Cre;Smo<sup>fl/fl</sup>* mice would be important to verify this idea. Furthermore, analyzing mice that express the constitutively active form of *Smo*, *Smo-A1*, (Hallahan et al., 2004) to determine if there is a similar phenotype to iHBC-Gli2 $\Delta$ N mice could also confirm the role of *Smo* in HBC regulation and olfactory regeneration. Together, these data suggest a SMO-independent and possible GLI-dependent role for HH in regulation of HBCs and olfactory neurogenesis. Additional mice need to be analyzed to confirm these preliminary findings.

An important component of the pathway that needs further investigation is the HH ligand and its source. SHH is the only member of the HH family that continues to be

expressed in the adult brain (Traiffort et al., 2010). Under normal conditions, neurons appear to be the main SHH-secreting cell type (as opposed to SHH-responding cells, which are primarily of glial nature), however, following injury, SHH expression has been reported in reactive astrocytes (reviewed in Petrova and Joyner, 2014). Along with other neuronal populations, it is possible that anterograde movement of SHH protein along axons allows the delivery of the protein to both the SVZ and striatum (reviewed in Petrova and Joyner, 2014). My preliminary data show that through *in situ hybridization*, SHH ligand might be present in SUS cells (Fig. 4-7A), however, in *Shh-Cre;Rosa26R-TdTomato* mice, in which *Shh* expressing cells and their progeny express TdTomato, clusters of cells including SUS cells, OSNs, and GBCs are positive for TdTomato (Fig. 4-7B-C). If SUS cells express *Shh*, it would coincide with the possible communication between SUS cells and HBC cilia. However, due to studies demonstrating secretion of SHH in neurons and that SHH protein can move along axons along with the detection of *Shh* in the OB (Gong et al., 2009), it is possible that the source can come from the bulb or OSNs. Analyzing the OE of *Shh-Cre;Rosa26R-TdTomato* mice or using *in situ hybridization* for the detection of *Shh* transcript following an injury could also elucidate the source of ligand in the OE.

What remains unknown is if the regulation of HBCs occurs in a true HH ligand-independent manner. The use of conditional *Ptch1<sup>fl/fl</sup>* (Ellis et al., 2003; Uhmman et al., 2007) mice could be used to specifically delete *Ptch1* from HBCs to support the theory that regulation of HBCs occurs in a HH-independent manner. Inhibition of SHH ligand with the antibody 5E1, can be administered to mice via an I.P. injection (O'Toole et al., 2011) to determine if normal OE homeostasis and regeneration following an injury is



disrupted. Additionally, HBCs can be cultured and treated with either 5E1 or SHH ligand to see if differentiation is inhibited or initiated respectively via immunofluorescence or qRT-PCR. In these cultured cells, other growth factors that have been implicated in GLI-dependent signaling can also be utilized to inhibit or drive differentiation. Furthermore, the GLI small-molecule inhibitor, GANT61 (Mazumdar et al., 2011), can be used *in vivo* or in cultured cells to specifically inhibit GLI activity to further elucidate the possible GLI-dependence of HBC regulation and regeneration in the OE.

### *Canonical Role for Hedgehog Signaling in the Olfactory Epithelium*

Interestingly, in mice treated with LDE-225, there was a reduction in attractive odor behaviors with no effect on aversive behaviors, specifically the fear-inducing compound from fox feces, TMT (Fendt and Endres, 2008) (Fig. 4-8). Various studies suggest that HH signaling is important for axon branching and targeting of OSNs to the OB and as before-mentioned, mature OSNs express *Ptch1*. It is possible that inhibiting the HH pathway affects the targeting of OE to affect specifically attractive odor behaviors. OSNs that express specific odorants target specific areas of the OB. The olfactory epithelium can be divided into two non-overlapping areas: a dorsal zone and a ventral one which can map to corresponding dorsal and ventral areas of the OB (Kobayakawa et al., 2007). Different odors were shown to map to different areas of the OB, for example, TMT activated glomeruli in the ventral domain of the OB (Kobayakawa et al., 2007). When OSNs from a specific domain were genetically deleted, mice became attracted to smells that were usually aversive, including TMT and certain attractive odors such as urine and peanut butter became aversive (Kobayakawa et al., 2007).

Because *Ptch1* is expressed in OSNs with regional variability, it is most likely that LDE-225 treatment affected only those neurons that express *Ptch1* which could coincide with OSNs that express specific odorant receptors responsible for detection of attractive odorants as opposed to aversive ones. Further analysis of additional odorants and specific domain markers of the OB to determine if there is still activity (TH expression) in mice treated with LDE-225 would help further elucidate the role of HH signaling in olfactory behavior. Additionally, analyzing a loss of *Ptch1* expression following LDE-225 via treatment in *Ptch1<sup>lacZ/+</sup>* mice would be important to ensure that treatment is effectively inhibiting the HH pathway in OSNs since *Ptch1* is a known readout of the pathway. Furthermore, cell-specific knockouts of other HH components in mature OSNs via the *OMP-Cre* allele and SUS cells via *K18-Cre* allele could provide additional information about the role of the HH signaling pathway in the OE.

Together, these experiments could elucidate a GLI-dependent role for the HH pathway plays in regulation of HBCs and olfactory neurogenesis and the HH ligand-dependent role in olfactory transduction and behavior.

#### *What Happens to Hedgehog Pathway Components in Mice that Lack HBC Cilia?*

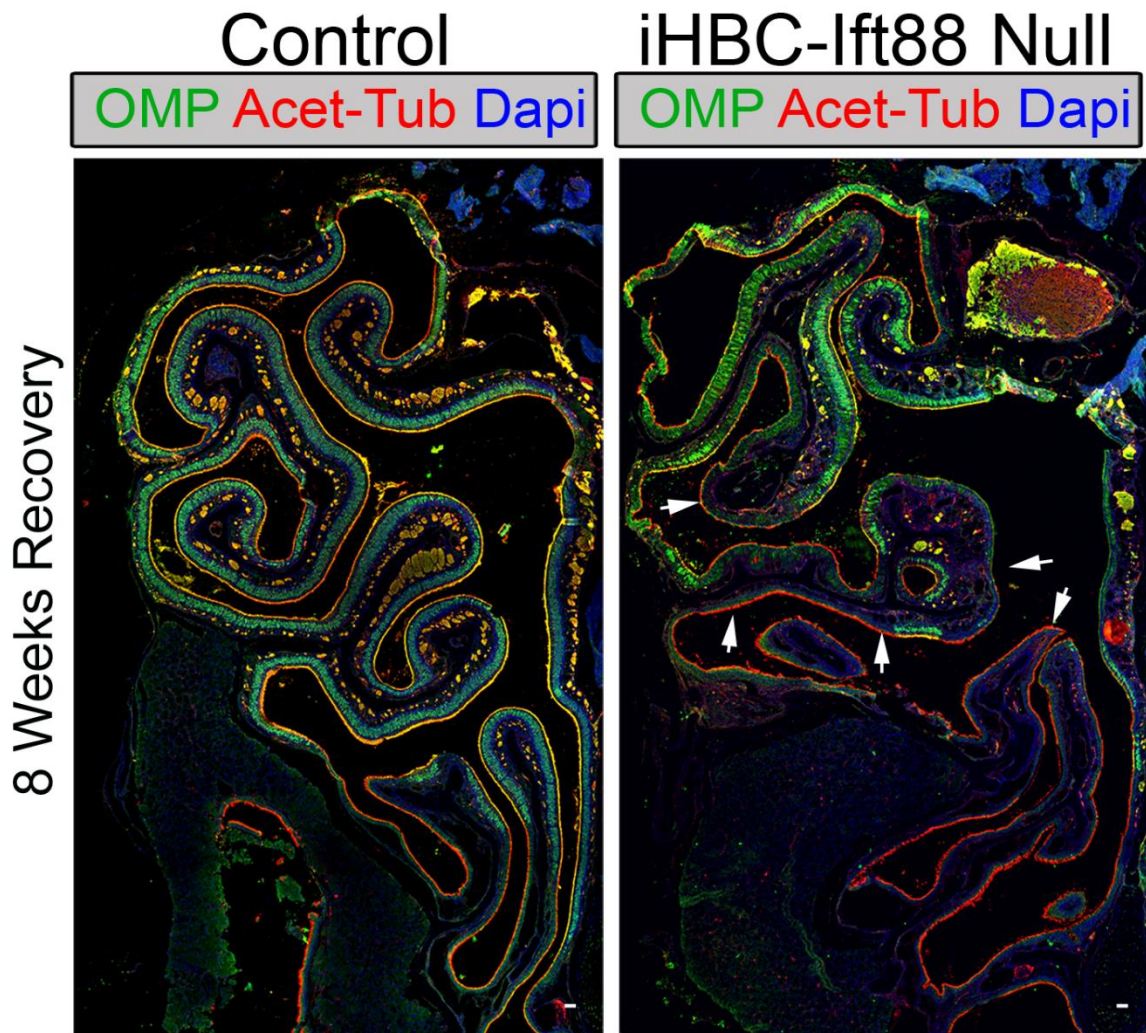
The HH pathway is tightly linked to primary cilia (Haycraft et al., 2005). Because HBCs possess cilia and the transcription factor GLI2, which localizes to tips of cilia, it would be important to investigate what happens to GLI2 and other HH components in iHBC-IFT88 null and iHBC-ARL13B null mice. Loss of *Arl13b* and *Ift88* have been shown to affect the HH pathway (Haycraft et al., 2007; Larkins et al., 2011). These null mice can be crossed with *lacZ* reporter mice that express specific HH components to determine what happens to the components after a loss of *Arl13b* or *Ift88*. It would be interesting to

see what happens in iHBC-IFT88 null and iHBC-ARL13B null mice that are crossed with iHBC-Gli2 $\Delta$ N mice and administered an injury to the OE. Without cilia, the constitutively active form of GLI2 could drive activation of HBCs regardless of the inability to detect the injury. Additionally, because *Sec8* is upregulated following injury to the OE, conditional deletion of *Sec8* or overexpression of *Sec8* in HBCs of control mice or cilia deficient mice could also elucidate its role and sufficiency in mediating the HBC to GBC transition following an injury to the OE. Without *Sec8*, HBCs may not be able to differentiate and regenerate the OE but its overexpression in iHBC-IFT88 null and iHBC-ARL13B null mice could bypass the loss of HBC cilia, allowing for proper differentiation. Furthermore, Notch and Wnt signaling pathways have been implicated in olfactory neurogenesis so analyzing these pathways along with HH *in vivo* or in cultured cells that either possess cilia or lack cilia can further elucidate what drives certain cell fates in the OE.

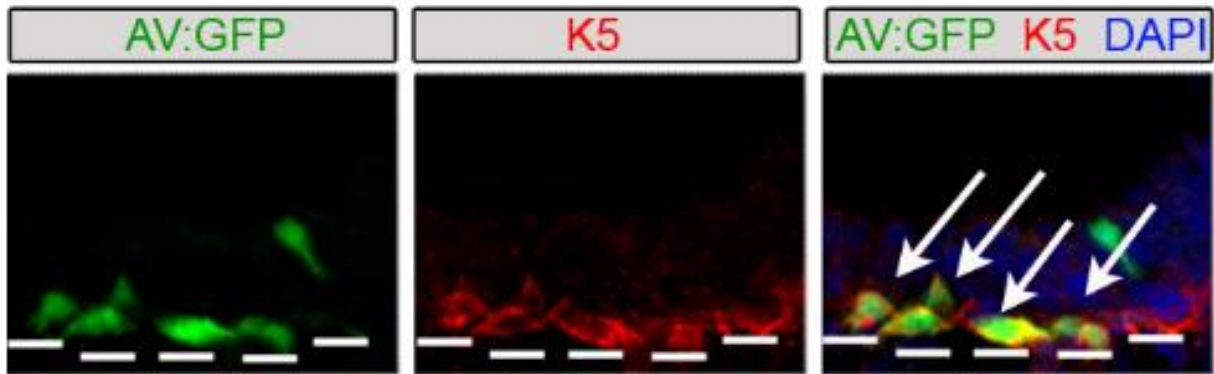
Overall, data presented in this dissertation demonstrate that HBCs, the presumed stem cell population of the OE, possess primary cilia and HH components that are important for HBC regulation and contribution to neurogenesis in the OE. My results provide novel insight on the mechanisms involved in regeneration of the OE by the introduction of a new role for cilia and the HH pathway in the olfactory periphery and the proposal of a GLI-dependent regulation of HBC activation and differentiation. There is most likely interplay between cilia and the HH pathway in regulating HBCs. Therefore, if olfactory dysfunction arises due to the loss of basal stem cell activity from loss of cilia due to a diseased state like a ciliopathy or aging or from a disruption in GLIs, restoration of cilia function or HH signaling components could be an important therapeutic tool.

Ultimately, these results establish a platform for future investigation of olfactory stem cell regulation.

### 4.3 Figures

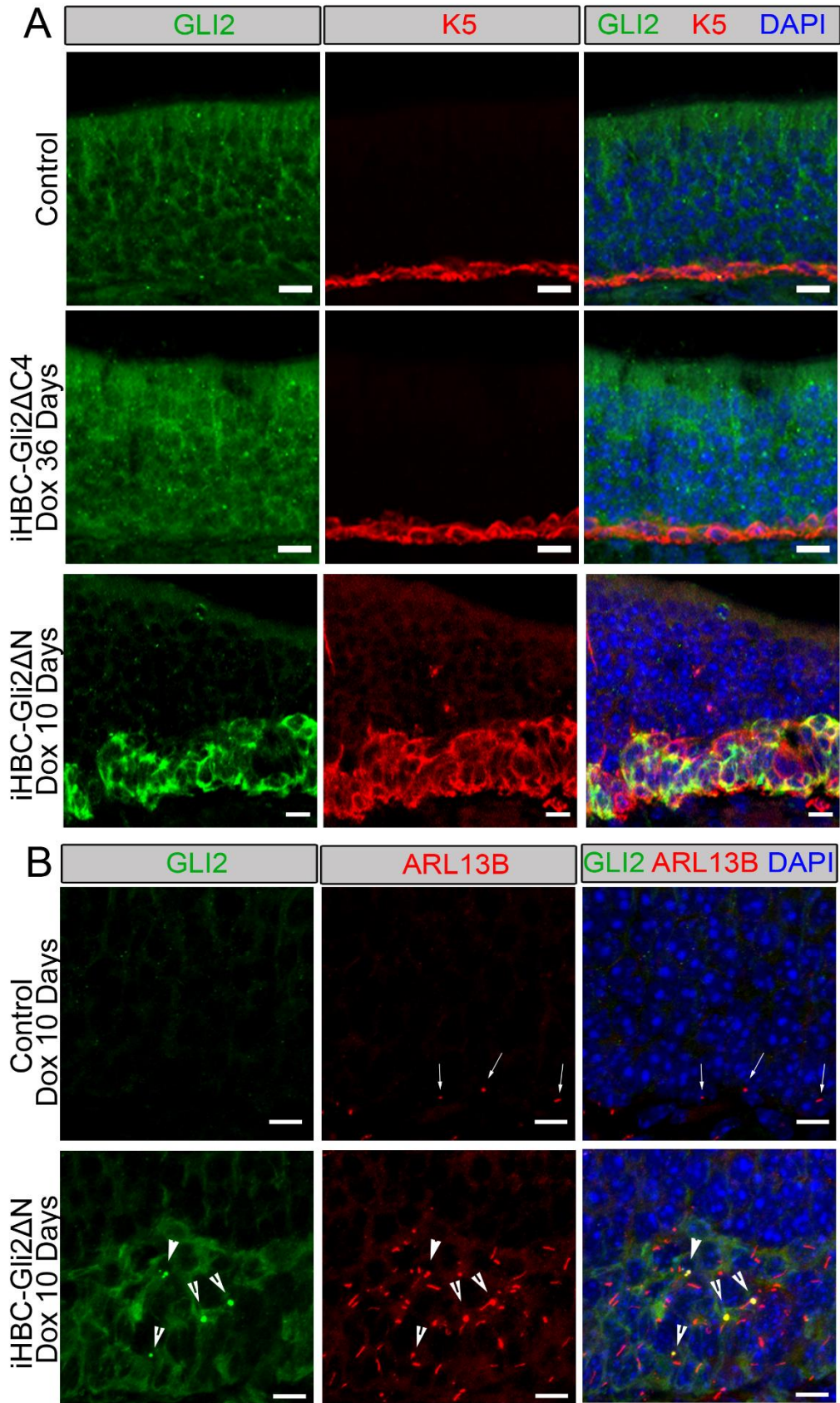


**Figure 4-1. Loss of HBC cilia results in respiratory infiltration.** Whole sections of the OE of control and iHBC-IFT88 null mice show respiratory infiltration (arrows) in iHBC-IFT88 null mice where Acet-tub labeled cilia are present in areas that lack OMP-labeled mature OSNs.



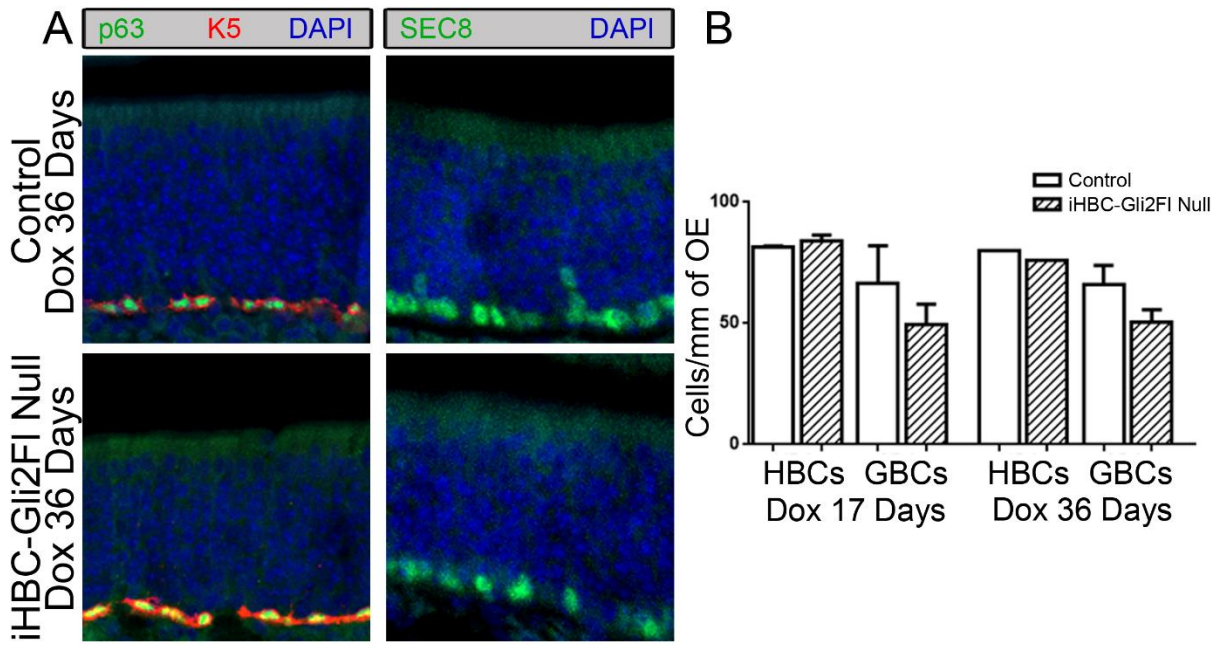
**Figure 4-2. HBCs are amenable to adenoviral infection.** Two days post MMI-induced injury to the OE, K5+ HBCs are infected with adenovirus (AV) containing GFP, AV:GFP (see arrows).



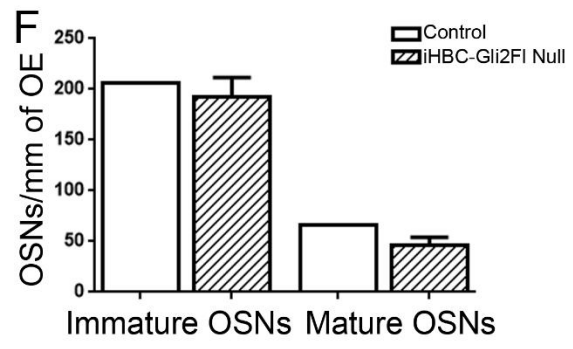
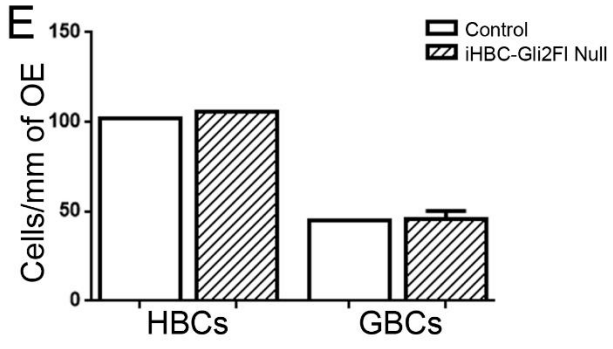
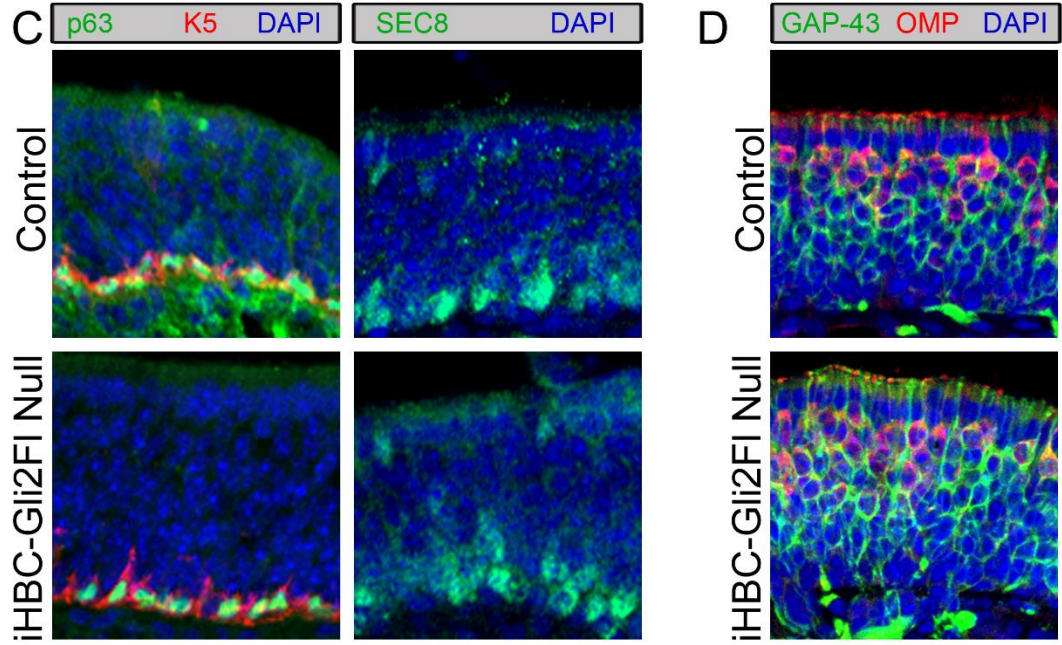


**Figure 4-3. GLI2 antibody detects Gli2 $\Delta$ N in cilia of HBCs but not endogenous GLI2 or Gli2 $\Delta$ C4.** Immunofluorescence analysis reveals (A) GLI2 antibody is co-expressed with K5+ HBCs of iHBC-Gli2 $\Delta$ N mice treated with dox for 10 days but not control or iHBC-Gli2 $\Delta$ C4 mice treated with dox for 36 days and (B) GLI2 antibody localizes to cilia of K5+ HBCs (see arrows) in iHBC-Gli2 $\Delta$ N mice treated with dox for 10 days but not control mice.

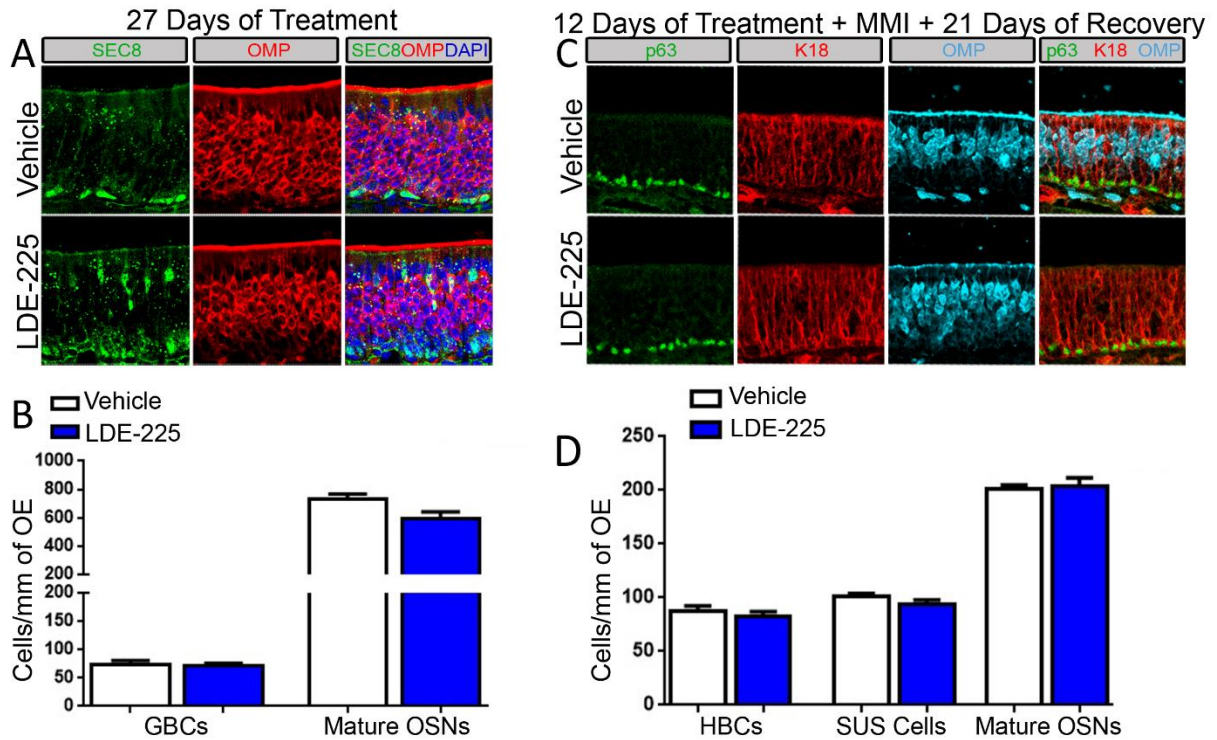




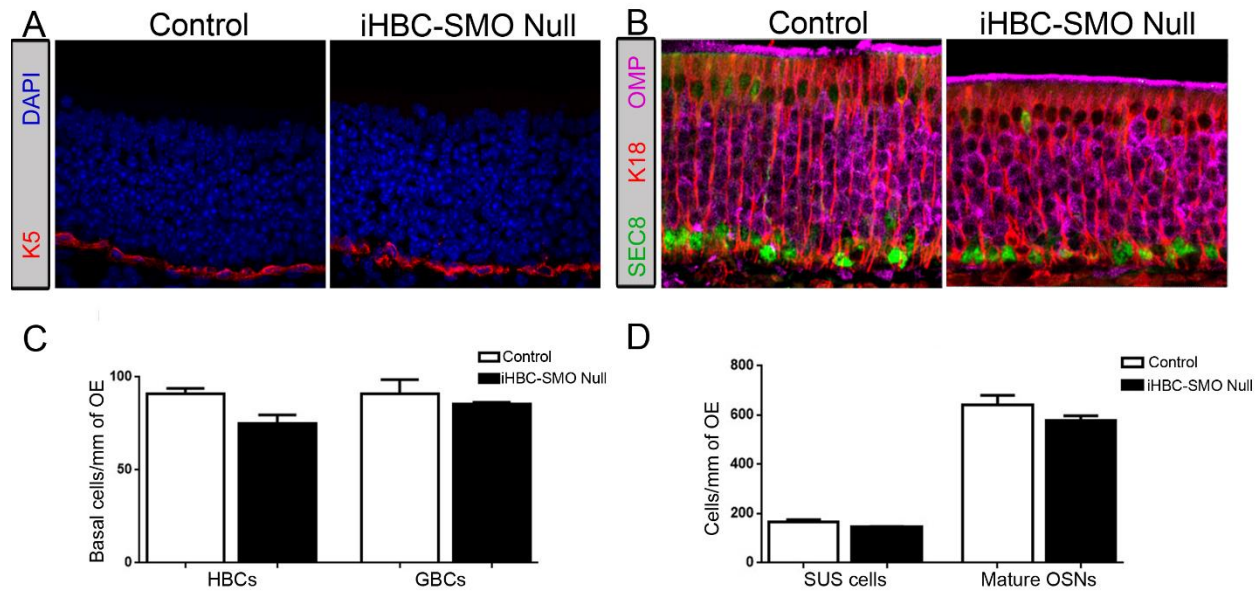
Dox 17 Days + Mx + 14 Days of Recovery



**Figure 4-4. Conditional loss of *Gli2* in HBCs has no effect on homeostasis or regeneration of the OE.** (A) Immunofluorescence analysis and (B) quantified data reveal that iHBC-*Gli2* null mice treated with dox for 17 or 36 days show no difference in the number of p63+/K5+ HBCs and SEC8+ GBCs compared to control mice. In iHBC-*Gli2* null and control mice treated with dox for 17 days and then administered an MMI-induced injury to the OE, (C, E) the number of p63+/K5+ HBCs and SEC8+ GBCs is similar as well as (D, F) the number of GAP-43+ immature and OMP+ mature OSNs.

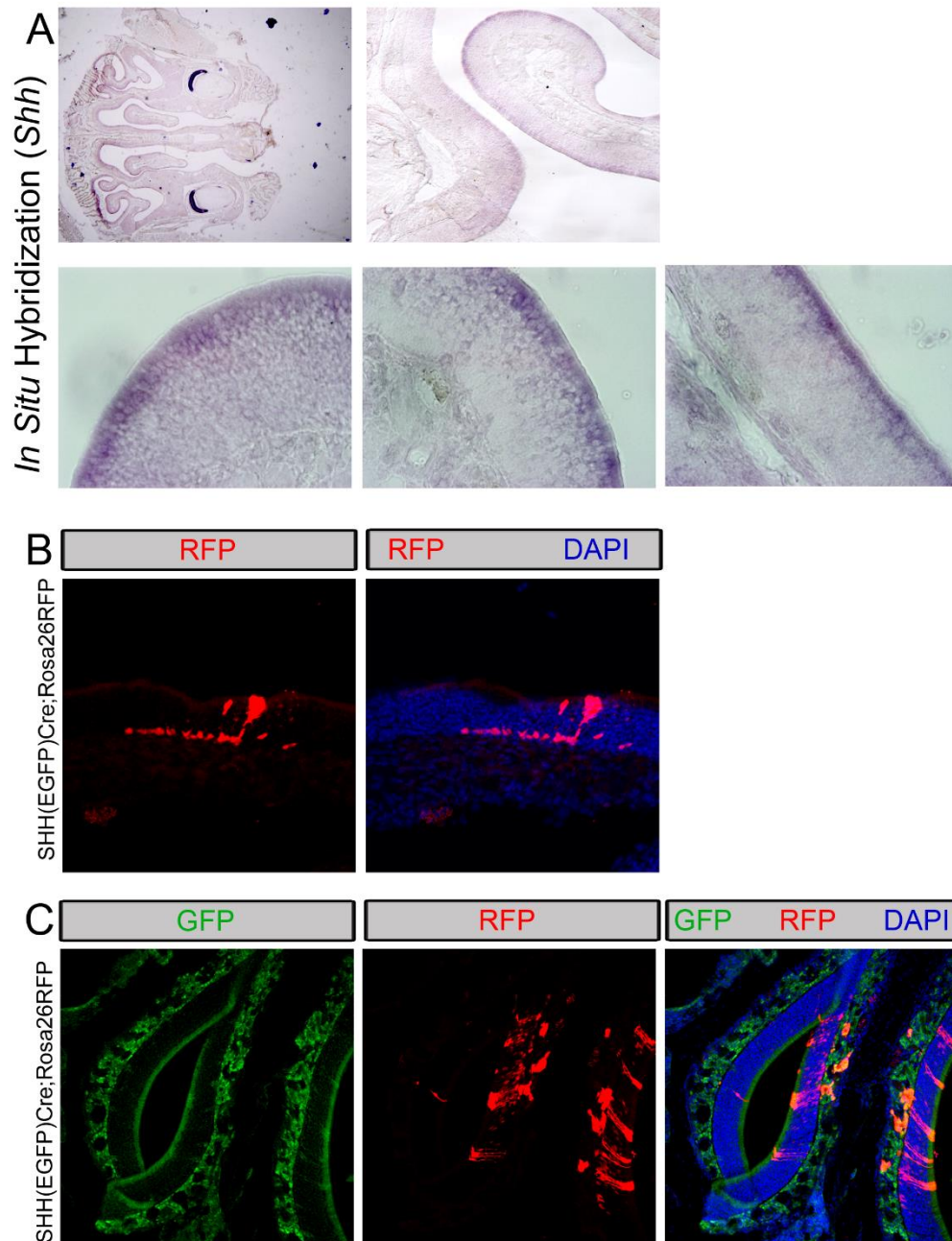


**Figure 4-5. The selective SMO inhibitor, LDE-225, has no effect on homeostasis or regeneration of the OE.** Mice treated with LDE-225 for 27 days exhibit (A-B) no difference in the number of Sec8+ GBCs or OMP+ mature OSNs compared to vehicle treated mice. Mice treated with LDE-225 for 12 days, administered an MMI-induced injury to the OE, and then allowed to recover for 21 days, exhibit (C-D) no difference in the number of p63+ HBCs, K18+ SUS cells, and OMP+ mature OSNs compared to vehicle treated mice.

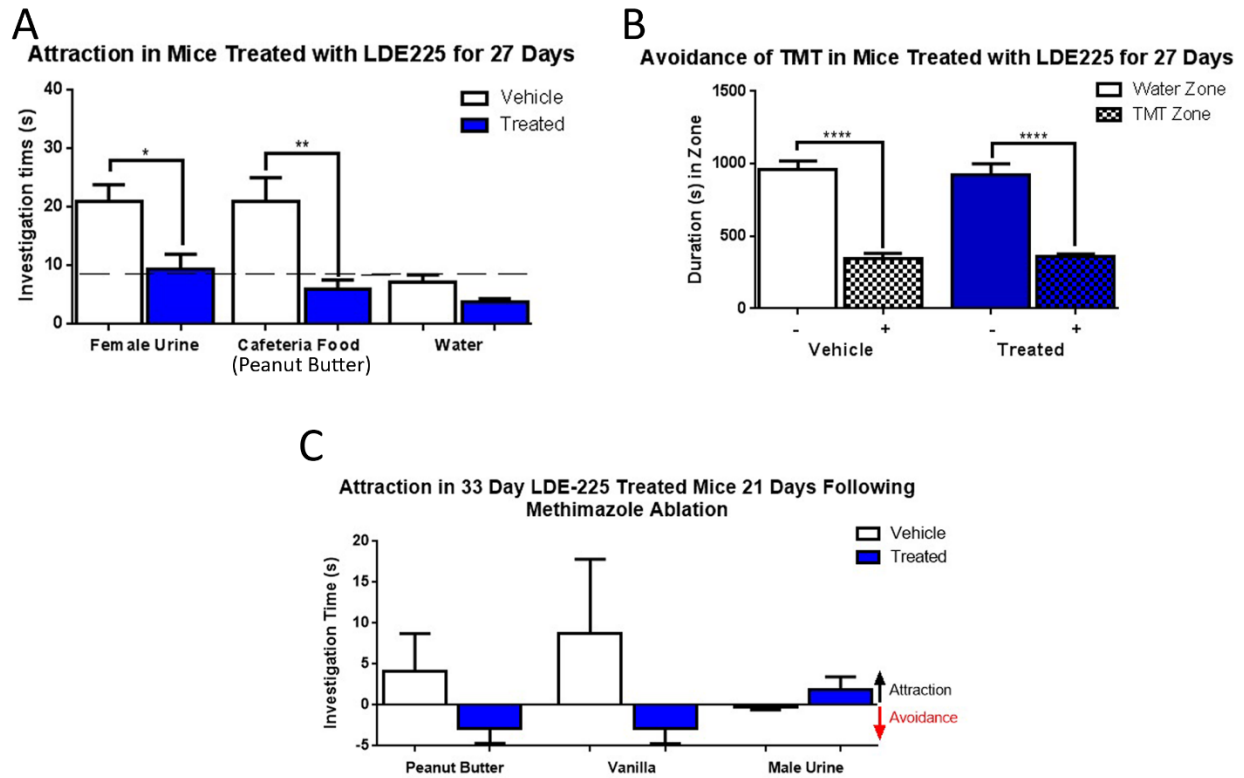


**Figure 4-6. Conditional loss of *Smo* in HBCs has no effect on homeostasis of the OE.** In iHBC-SMO null mice treated with dox for 19 days there is (A,C) no difference in the number of K5+ HBCs and (B, C-D) no difference in the number of SEC8+ GBCs, K18+ SUS cells, and OMP+ mature OSNs compared to control mice.





**Figure 4-7. *Shh* might be present in SUS cells of the OE.** (A) *In situ* hybridization of control tissue with RNA probe against *Shh* shows expression of the transcript in the tooth bud (internal control) and SUS cells of the OE. In *ShhCreER;Rosa26RFP* mice, (B) RFP signal is seen in basal cells and SUS cells while (C) GFP is expressed specifically in SUS cells, suggesting they are the source of SHH, and RFP is expressed in SUS cells, OSNs, BG cells, and basal cells, suggesting they are the progeny.



**Figure 4-8. The selective SMO inhibitor, LDE-225, reduces attractive behaviors in mice during homeostasis and following injury.** (A) Mice treated with LDE-225 for 27 days show a reduction in the investigation time for the attractive odors, urine and peanut butter, but (B) show no difference in avoidance of the component of fox feces, TMT, compared to vehicle treated mice. (C) Mice treated with LDE-225 for 12 days, administered an MMI-induced injury to the OE, and then allowed to recover for 21 days, exhibit a reduction in the investigation time for the attractive odors, peanut butter and vanilla compared to vehicle treated mice.

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