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BRAIDing receptors for cell-specific targeting

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Abstract

Systemic toxicity is a major challenge in the development of therapeutics. Consequently, cell-type-specific targeting is needed to improve on-target efficacy while reducing off-target toxicity. Here, we describe a cell-targeting system we have termed BRAID (**BR**idged **A**ctivation by **I**ntra/intermolecular **D**ivision) whereby an active molecule is divided into two inactive or less active parts that are subsequently brought together via a so-called 'bridging receptor' on the target cell. This concept was validated using the WNT/β-catenin signaling system, demonstrating that a multivalent WNT agonist molecule divided into two inactive components assembled from different epitopes via the hepatocyte receptor βKlotho induces signaling specifically on hepatocytes. These data provide proof-of-concept for this cell-specific targeting strategy and in principle, this may also allow activation of multiple signaling pathways where desirable. This approach has broad application potential for other receptor systems.

eLife assessment

This **important** study presents a new way to selectively activate a cell signaling pathway in a specific cell type by designer ligands that link signaling co-receptors to a marker specific to the target cells. **Convincing** experimental results demonstrate that the agonist molecules activate Wnt signaling in target cells expressing the marker as intended. More broadly, this concept could be used to induce Wnt signaling or another pathway initiated by co-receptor association in a cell type-specific manner. In vitro results in this study could be further strengthened by assessing the biological consequences of Wnt activation in target cells.

Introduction

Receptor-mediated signaling is fundamental to cell–cell communication, regulation of cellular growth/differentiation, maintenance of tissue function/homeostasis, and regulation of injury repair. When a cell-specific response is necessary, nature achieves that selectivity through various mechanisms such as cell-specific receptors, ligand gradient, short-range ligands, and direct cell–cell contacts. However, most ligand receptor systems have pleiotropic effects due to the broad

expressions of receptors on multiple cell types. While this may be important when a coordinated response in multiple cell types or tissues is needed, achieving cell-specific signaling to avoid systemic toxicity or off-target effects remains a major challenge in both research and therapeutic development. In addition, it is often difficult to identify differences between normal and diseased cells for a particular signaling pathway of interest, making it challenging, if not impossible, to modulate that signaling pathway selectively in either diseased or normal cells. Therefore, methods for effective cell targeting are needed for both research and therapeutic development.

Compared with cell-targeted antagonists, cell-targeted agonists are more complex to design. In addition to cell targeting, agonist molecules are also subject to stringent requirements in terms of affinity, epitope, and geometry (Dickopf et al., 2020). Previous efforts to engineer cell-selective growth factors and cytokines have employed various approaches, such as the "chimeric activators" concept (Cironi et al., 2008), where a cell-targeting arm ("targeting element") is attached to either the wild-type ligand or a mutated ligand with reduced affinity toward the signaling receptor ("activity element"). Such an approach has been applied to several signaling pathways, such as those based on erythropoietin (Taylor et al., 2010; Burrill et al., 2016), interferons (Cironi *et al*., 2008; Garcin et al., 2014), and interleukin-2 (Ghasemi et al., 2016; Lazear et al., 2017). While some selectivity has been achieved by attaching a targeting arm to a wild-type ligand, up to 1000-fold selectivity has been achieved using a mutated ligand (Garcin *et al*., 2014).

The "chimeric activators" approach is based on the cooperativity concept, where mutations that weaken the affinity of a natural ligand to its receptor are selected as the "activity element". Due to this weakened affinity, the mutant "activity element" alone displays a significantly right-shifted dose–response curve (i.e., lower potency) in an activity assay, for both target and non-target cells that express the signaling receptors. When the "targeting element" is tethered to the mutant "activity element", the "targeting element" helps to increase the local concentration of the mutant "activity element" on the desired target cell surface. This combination drives engagement of the signaling receptor and subsequent intracellular signaling activation, left-shifting the dose–response curve (i.e., higher potency) on the target cell and creating a separation between target vs. non-target cells. While conceptually elegant, identifying the appropriate mutations that achieve the precise reduction of affinity to be rescued by the "targeting element" is not trivial. In some cases, while the potency could be rescued, the maximal signaling strength remained compromised, resulting in a partial agonist. In addition, the selectivity is not exquisite, with most literature examples reporting a modest 10-fold separation between target vs. non-target cells. Additional strategies that show promising results have also been reported; for example, inactive pro-drugs that require tumor-associated proteases for activation (Puskas et al., 2011; Skrombolas et al., 2019); complementation of two inactive components via targeted assembly in trans (Banaszek et al., 2019); and passive enrichment on the target cell leading to colocalization of monomeric subunits (Mock et al., 2020) or inactive "split" components (Quijano-Rubio et al., 2022).

Here, we present a novel concept to achieve cell targeting for ligand/receptor systems that involves multicomponent receptor complexes, where a productive signaling competent receptor complex is directly assembled through a "bridging element". We have tested this concept using the WNT/β-catenin signaling pathway as a model system.

The WNT pathway is highly conserved across species and crucial for embryonic development as well as adult tissue homeostasis and regeneration (Nusse and Clevers, 2017). WNT-induced signaling through β-catenin stabilization has been widely studied and is achieved by the ligand binding to frizzled (FZD) and the low-density lipoprotein receptor-related protein (LRP) families of receptors. There are 19 mammalian WNTs, 10 FZDs ($FZD_{1\text{-}10}$), and two LRPs (LRP5 and LRP6). WNTs are highly hydrophobic due to lipidation, which is required for them to function, and they are promiscuous, capable of binding and activating multiple FZD and LRP pairs (Janda et al.,

2012; Kadowaki et al., 1996; Dijksterhuis et al., 2015). Elucidating the functions of individual FZDs in tissues has been hampered by difficulties in producing the ligands and their lack of receptor and tissue selectivity. Recent breakthroughs in the development of WNT-mimetic molecules have largely resolved the production and receptor-specificity challenges (Janda et al., 2017; Chen et al., 2020; Tao et al., 2019; Miao et al., 2020). Although tissue selectivity has been partly achieved by tissue injury (damaged tissues seem more sensitive to WNTs (Xie et al., 2022)), the ability to target WNTs to specific cells and tissues would be a significant technical and therapeutic advancement.

The WNT mimetics reported so far are all bispecific and can simultaneously bind to FZDs and LRPs, and their optimal stoichiometry (at least for the antibody-based molecules) are tetravalent bispecific (2:2 format), requiring two FZD binders and two LRP binders in the same molecule to achieve efficient signaling (Tao *et al*., 2019; Chen *et al*., 2020). We have taken advantage of the fact that two FZD binders alone and two LRP binders alone do not signal. Cell specificity may be achieved by attaching a "targeting element" (capable of binding to another cell surface receptor, called a bridging receptor here) to these two inactive molecules. Signaling-competent receptor complexes consisting of two FZDs and two LRPs could then be assembled via the bridging receptor on the target cell surface. This approach reduces or eliminates the need to mutate and reduce the affinity of the "active elements" towards the signaling receptor, and creates a highly cell specific activation of the signaling pathway as the individual components are inactive. A detailed proof-of-concept study based on the WNT/β-catenin signaling pathway is presented herein. We have termed the use of cell-targeted WNT mimetics SWIFT (**S**plitting of **W**NT to **I**nduce **F**unctional **T**argeting).

Results

Conceptual design of cell-targeted activators via a bridging receptor

Figure 1A shows one optimized design for a WNT mimetic that is a tetravalent bispecific antibody-based molecule. It is important to note that efficient WNT/β-catenin signaling requires two FZD binding domains and two LRP binding domains in one molecule (Chen *et al*., 2020). **Figure 1B** shows a cell-targeting approach using the bridging receptor concept, i.e., the SWIFT approach. The first step of this concept is to split the active molecule into inactive components. In the case of the tetravalent bispecific WNT mimetic, the active molecule is split into one molecule having two FZD binding arms and a second molecule having two LRP binding arms. These two inactive components are then each tethered to a different "bridging element" binding to a different epitope on the same bridging receptor (the tethered molecules named αLRP-αBR-1 and αFZD-αBR-2 in **Fig. 1B**, top two panels). αLRP-αBR-1 and αFZD-αBR-2 are each inactive on non-targeting cells where the bridging receptor is not expressed (**Fig. 1B** top panels). On targeting cells where the bridging receptor is expressed, FZD and LRP are then assembled or brought into proximity with one another by αLRP-αBR-1 and αFZD-αBR-2 via the bridging receptor, recreating the signaling-competent receptor complex (**Fig. 1B** bottom panel).

Proof of concept with the targeted WNT mimetic molecules

To test the concept shown in **Fig. 1B**, we selected the βKlotho and endocrine fibroblast growth factor 21 (FGF21) ligand system as the bridging receptor system. FGF21 is an endocrine hormone produced by the liver that regulates metabolic homeostasis (BonDurant and Potthoff, 2018). FGF21 signals through FGFR1c, FGFR2c, and FGFR3c in the presence of co-receptor βKlotho (Zhang and Li, 2015). The binding of FGF21 to the receptor complex is primarily driven by its affinity toward βKlotho via its C-terminal domain (Lee et al., 2018; Shi et al., 2018), while its N-

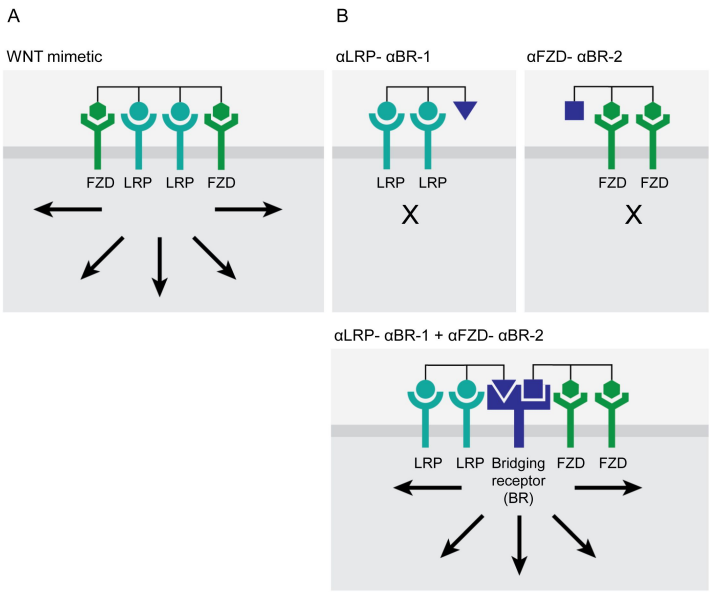

Figure 1.

Activation of a signaling pathway by split molecules through binding to a bridging receptor on the target cell surface.

A) Efficient WNT/β-catenin signaling requires two FZD binding domains and two LRP binding domains in one WNT mimetic molecule. B) WNT mimetic molecule is split into one molecule having two FZD binding arms (2:0) and a second molecule having two LRP binding arms (0:2) and then each tethered to a different "bridging element" binding to a different epitope on the same bridging receptor (named αLRP-αBR-1 and αFZD-αBR-2) (top two panels). On target cells where the bridging receptor is expressed, FZD and LRP are then assembled by αLRP-αBR-1 and αFZD-αBR-2 via the bridging receptor, recreating the signaling-competent receptor complexes (bottom panel). Arrows indicate activation of WNT/β-catenin signaling.

terminal domain is important for FGFR interaction and signaling (Yie et al., 2012; Micanovic et al., 2009). βKlotho-binding antibodies that could induce βKlotho/FGFR signaling have also been identified, and one particular agonistic βKlotho antibody binds to a different epitope on βKlotho from FGF21 and does not compete with FGF21 binding (Min et al., 2018). Therefore, the following bridging receptor (βKlotho) binding elements were selected to test the cell-targeting SWIFT concept:

- FGF21FL (full length FGF21) that can bind to βKlotho and induces FGFR signaling
- FGF21ΔC (FGF21 without the C-terminal βKlotho interaction domain) that does not bind βKlotho nor is capable of inducing FGFR signaling
- FGF21ΔN (FGF21 without the N-terminal FGFR interaction domain) that binds βKlotho but does not signal
- FGF21ΔNΔC that cannot bind βKlotho and cannot signal
- 39F7 IgG that binds βKlotho, to a different epitope from FGF21, and can induce FGFR signaling

The FZD- and LRP-binding domains selected were F (binds $FZD_{1,2,5,7,8}$) and L (binds LRP6), previously termed F1 and L2, respectively (Chen *et al*., 2020). Graphic representations of the binders and their various combinations are shown in **Figs. 2A-C**.

To test the concept in **Fig. 1B**, the FZD binder (F) was combined with two versions of the bridging receptor (βKlotho) binder, F-FGF21FL and F-FGF21ΔN (**Fig. 2B**), and the LRP binder (L) was combined with the other bridging receptor (βKlotho) binder 39F7 as L-39F7 (**Fig. 2B**).

We first confirmed the binding of the various fusion molecules shown in **Fig. 2B** and **2C** to their respective target proteins. All F- and L-containing molecules bind to either FZD_7 or LRP6E3E4 fragments as expected (**Figs. 2D-J**). FGF21FL, FGF21ΔN, and 39F7 bind to βKlotho, while FGF21 without its C-terminal domain (FGF21ΔC and FGF21ΔNΔC) does not bind to βKlotho (**Figs. 2D-J**). Therefore, the molecule formats of the various fusion proteins have no significant impact on the individual element's binding to their target receptors.

Next, we performed Octet binding assays to assess whether F-FGF21 or L-39F7 allow simultaneous bindings to their target receptors. Sequential additions of the various F-FGF21 fusion molecules to the sensor surface, followed by FZD_7 CRD and then βKlotho show that a stepwise increase in binding signal is observed with FZD_7 CRD, and that F-FGF21FL and F-FGF21ΔN show additional binding to βKlotho but not F-FGF21ΔC nor F-FGF21ΔNΔC (**Fig. 2K**). This suggests that F-FGF21FL or F-FGF21ΔN are capable of simultaneous binding to both FZD_7 and βKlotho receptors.

Sequential additions of the various L, 39F7, and αGFP (a negative control antibody) combinations to the sensor surface followed by LRP6E3E4 and then βKlotho revealed a stepwise increase in binding signal with L-39F7 but not the other negative control molecules, αGFP-39F7 and L-αGFP (**Fig. 2L**). This suggests that L-39F7 can simultaneously bind to both LRP6 and βKlotho receptors.

The ability of this set of molecules to activate WNT/β-catenin signaling was assessed in WNT-responsive Huh7 and HEK293 Super TOP-FLASH (STF) reporter cells (Zhang et al., 2020). As shown in **Fig. 3B**, the combination of F-FGF21FL or F-FGF21ΔN with L-39F7 resulted in WNT/β-catenin signaling in Huh7 cells, a liver cell line that expresses the bridging receptor βKlotho (*KLB*), but not in HEK293 cells, where βKlotho is not expressed (**Fig. 3A** and **3G**). This signaling depends on the presence of both FZD and LRP binding arms and the ability to bind the bridging receptor, as the removal of the LRP binding arm L from L-39F7 or inactivation of βKlotho binding arms (use of FGF21ΔC or FGF21ΔNΔC, or the replacement of 39F7 with αGFP) removes activity in both cells (**Figs. 3A-F**). We further examined the target cell selective Wnt signal activation in a 2-layer cell culture system as depicted in **Fig. 3H**. In this co-culture system, two different cell types are separated by a permeable membrane, and the two different cell lines are stimulated with the

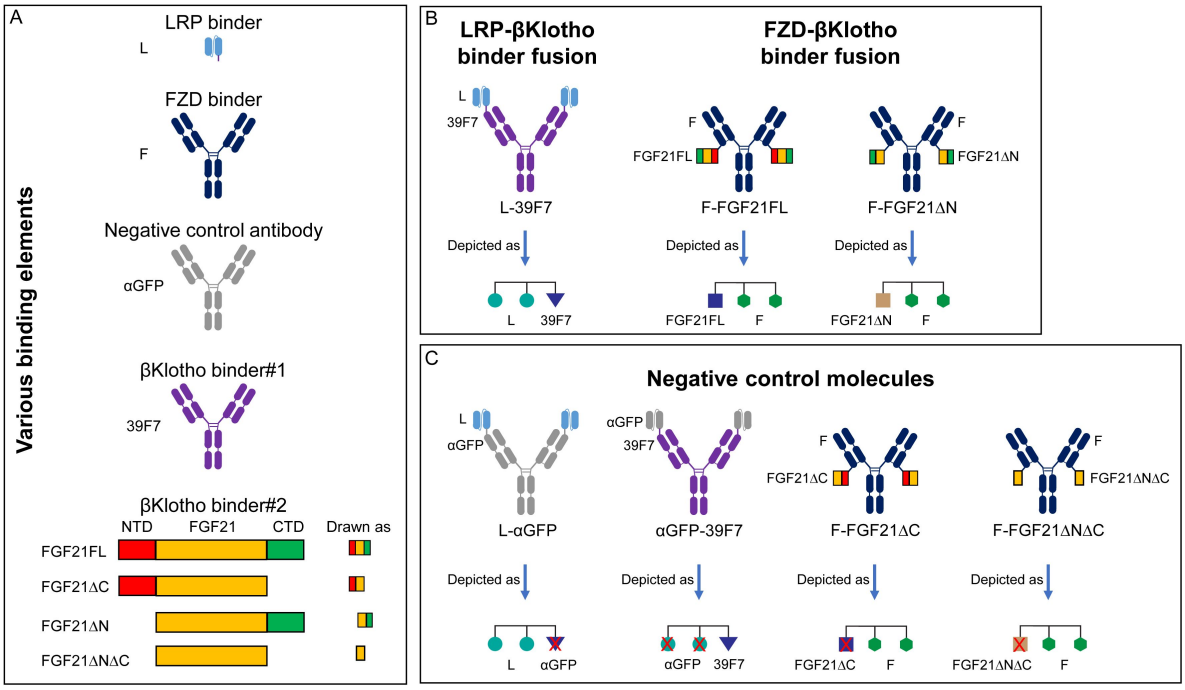

Figure 2.

Diagrams of the molecules used in the experiment to provide proof-of-concept for SWIFT.

A) Elements that are used in the split molecules. The LRP6 binder element is in scFv format; FZD binder is in IgG1 format; both αGFP IgG1 and αGFP scFv are used for assembly of the negative control molecules. Two types of βKlotho binders are used. Binder#1, 39F7 IgG1, a βKlotho monoclonal antibody; Binder#2, FGF21FL and different deletion variants. B) Assembled SWIFT molecules. C) Assembled negative control molecules. D–G) Bindings of various F-FGF21 fusion proteins to FZD_7 and βKlotho. Bindings of FZD_7 and β-Klotho to F-FGF21FL (D), F-FGF21ΔN (E), F-FGF21ΔC (F), or F-FGF21ΔNΔC (G) were determined by Octet. H–J) Binding of LRP6 and βKlotho to L-39F7 (H), αGFP-39F7 (I), or L-αGFP (J) were determined by Octet. Mean K_D values were calculated for the binding curves with global fits (red dotted lines) using a 1:1 Langmuir binding model. (K) Step bindings of FZD_7 and βKlotho to various F-FGF21 fusion proteins. Sequential binding of F-FGF21FL (blue sensorgram), F-FGF21ΔN (red sensorgram), F-FGF21ΔC (light-green sensorgram), or F-FGF21ΔNΔC (green sensorgram), followed by FZD_7 CRD, then followed by addition of βKlotho on Octet shows simultaneous engagement of both FZD_7 and βKlotho to the indicated F-FGF21 proteins. Sensorgrams for FZD_7 and βKlotho area (red dotted box) are enlarged at the right. (L) Step binding of LRP6 and βKlotho to L-39F7 and its control proteins. Sequential binding L-39F7 (blue sensorgram), L-αGFP (light-blue sensorgram), αGFP-39F7 (red sensorgram), or 39F7 IgG (green sensorgram), followed by LRP6E3E4, then followed by addition of βKlotho on Octet shows simultaneous engagement of both LRP6 and βKlotho to the indicated L-39F7 and its control proteins. Sensorgrams for LRP6 and βKlotho area (red dotted box) are enlarged on the right.

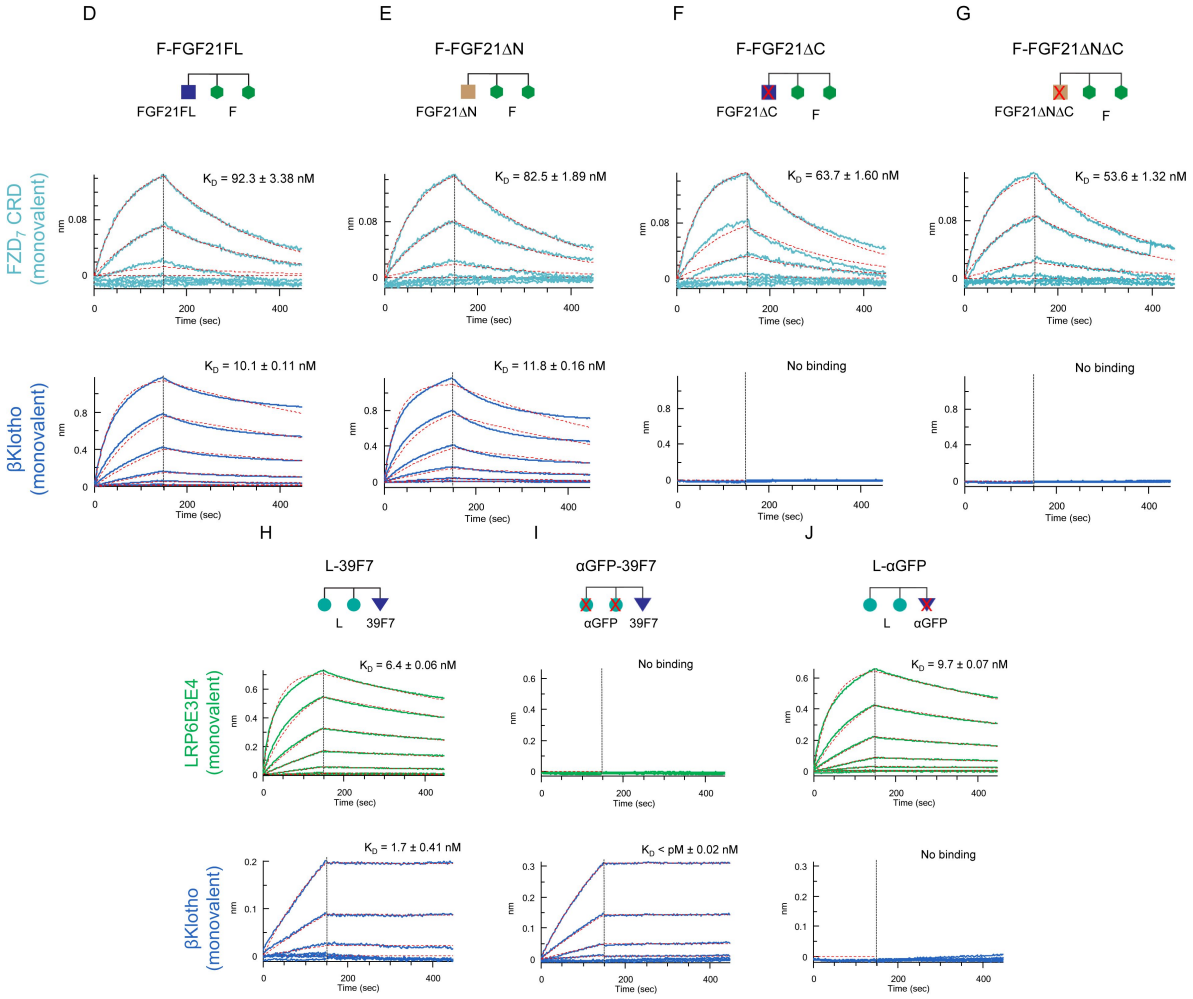

Figure 2. (continued)

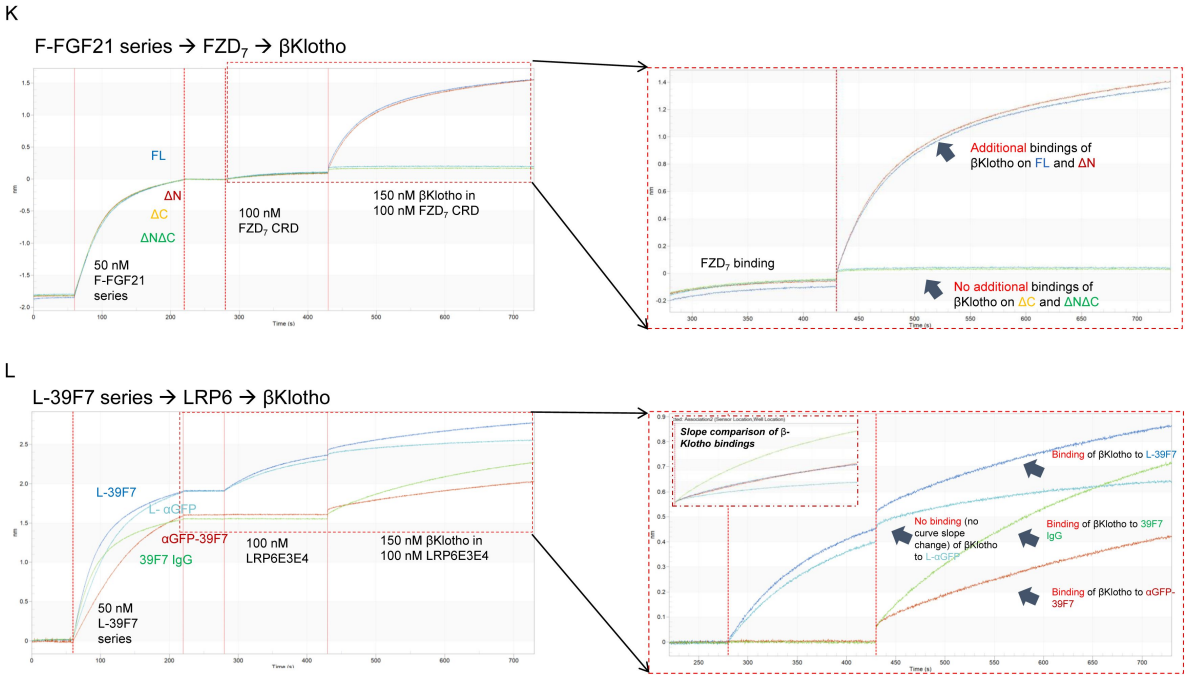

Figure 2. (continued)

same treatment medium in the same vessel. The combination of F-FGF21ΔN and L-39F7 showed a robust increase in WNT/β-catenin signaling in Huh7 cells as compared to the negative control mixture of F-FGF21ΔNΔC and L-39F7. The target cell specific WNT/β-catenin signaling activation was not detected in HEK293 cells (**Fig. 3H**). Whether plating cells in the upper or lower level of the co-culture system did not affect specificity or potency. These results provide experimental evidence supporting the SWIFT concept presented in **Fig. 1B**.

Validation of liver-specific targeting with primary human cells

To test the potency of these molecules in cells directly derived from the tissue of interest, we selected primary human hepatocytes and human small intestinal organoids (**Fig. 4A**). These cultures better represent the physiological and transcriptional characteristics of the liver and intestine compared to cell lines. As expected, primary human hepatocytes express bridging receptor βKlotho, while human small intestinal cells do not (**Fig. 4B**). The combination of F-FGF21ΔN and L-39F7 in human hepatocytes causes a significant increase in the expression of WNT target gene *AXIN2* after 24 h compared with the control (**Fig. 4C**). The combination with the negative control F-FGF21ΔNΔC does not upregulate *AXIN2*. The same panel of molecules does not elicit any target gene expression in human small intestinal cells, confirming the need for bridging receptor expression for activity (**Fig. 4D**). These results in primary cells support the feasibility of this cell-specific targeting strategy, and we expected them to be predictive of tissue specific *in vivo* responses.

Discussion

A major challenge in the development of new therapeutics is the effective targeting of drugs towards a desired cell type. Due to the pleiotropic expression and actions of most drug targets in many cell types/organs and the lack of differentiation between diseased vs. normal cells, many drugs exhibit either dose-limiting toxicity or act on multiple cell types of opposing activity, rendering them less effective. Therefore, developing effective cell-targeting methods would allow reduced systemic toxicity and higher efficacy for more effective treatments.

Herein, we have described a novel cell-targeting approach termed BRAID whereby an active drug molecule is divided into inactive parts that are assembled via a bridging receptor specific to the target cell. Although complementation and splitting a molecule into inactive parts have been explored previously, the novelty of our approach is that there is no requirement for the two split inactive components to interact with one another. Therefore, it does not require cooperative interactions between the split components and receptors for activity. In our approach, assembly of the signaling complex is achieved by simultaneous binding of the two divided inactive components through a common bridging receptor (**Fig. 1B**).

We tested this concept using the WNT/β-catenin signaling pathway as a model system. This signaling system requires two receptors, FZD and LRP. The present authors (and others) have generated antibody-based WNT mimetic molecules by linking FZD binders and LRP binders in a single molecule to activate the FZD/LRP receptor complex (Chen *et al*., 2020; Janda *et al*., 2017; Tao *et al*., 2019). To explore the BRAID concept with the WNT signaling receptors, we first divided a tetravalent bispecific WNT mimetic into two components, one containing two FZD binding domains and the other containing two LRP binding domains. To each of these two inactive components, a moiety that binds to the bridging receptor, in this case βKlotho (predominantly expressed in hepatocytes), was attached. The two bridging receptor binding moieties are FGF21 and 39F7, which bind to non-overlapping regions on βKlotho (Min *et al*., 2018). As demonstrated both on WNT-responsive reporter cell lines as well as on primary human hepatocytes and human intestinal organoids, target-cell-specific WNT signaling is indeed observed when the two inactive

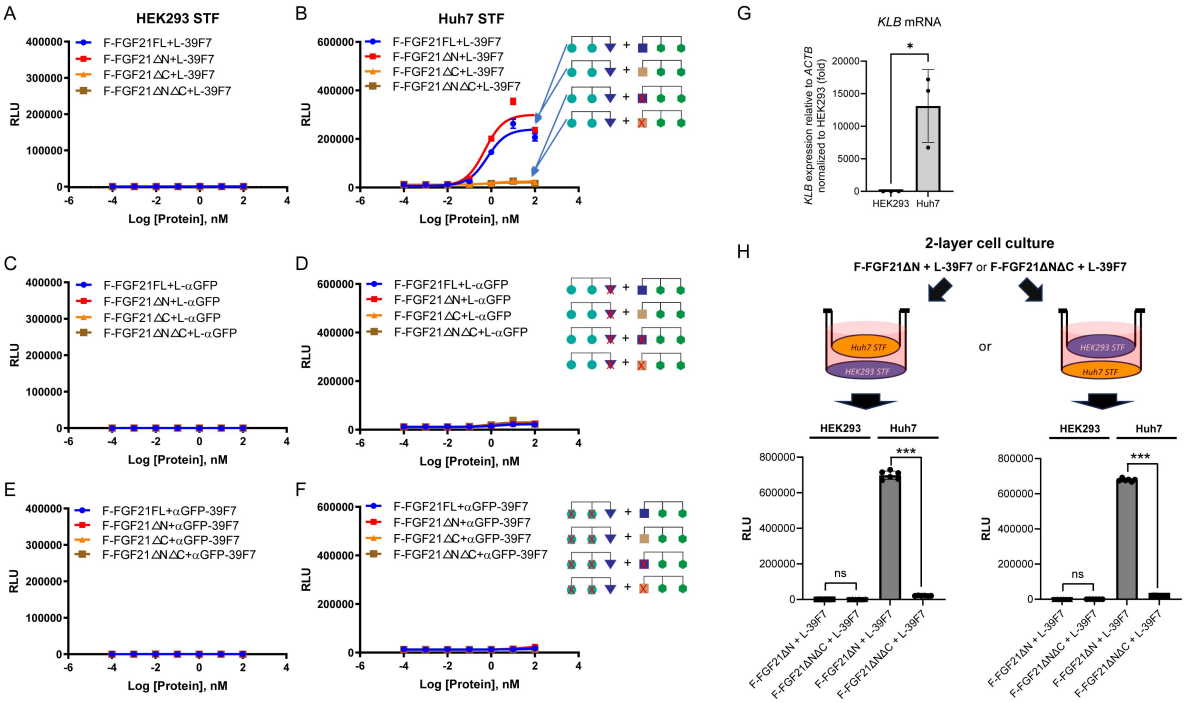

Figure 3.

Dose-dependent STF assay of SWIFT molecules in HEK293 and Huh7 cells.

A–F) Various F-FGF21 fusion proteins in the presence of L-39F7 in HEK293 STF cells (A) and Huh7 STF cells (B); various F-FGF21 fusion proteins in the presence of L-αGFP in HEK293 STF cells (C) and Huh7 STF cells (D); and various F-FGF21 fusion proteins in the presence of αGFP-39F7 in HEK293 STF cells (E) and Huh7 STF cells (F). G) Expression of bridging receptor βKlotho (*KLB*) in HEK293 and Huh7 cells normalized to *ACTB*, relative to HEK293 expression. H) STF responses in a 2-layer cell culture system after 16h treatment with 10 nM of indicated molecules. Data are representative of three independent experiments performed in triplicate and are shown as mean ± standard deviation (SD). **P*<0.05, ****P*≤0.001 (Unpaired t test)

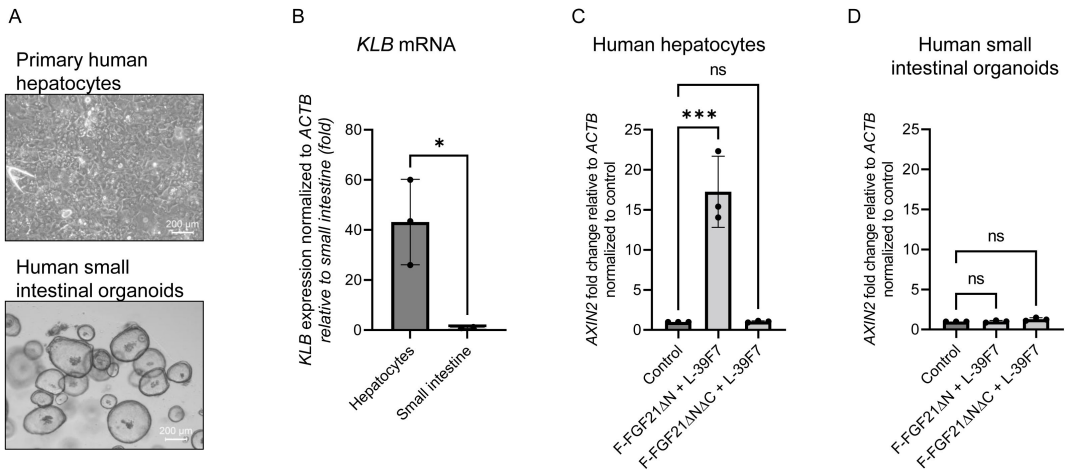

Figure 4.

Activity of targeted molecules in primary human cells.

A) Representative images of primary human hepatocyte cultures in 2D or human small intestinal organoids. Scale bar: 200 µm. B) Expression of bridging receptor βKlotho (*KLB*) in hepatocytes or small intestinal cells. C) WNT target gene *AXIN2* expression normalized to control treatment after 24-h treatment with 10 nM of the indicated molecules in human hepatocytes. D) WNT target gene *AXIN2* expression normalized to control treatment after 24-h treatment with 10 nM of the indicated molecules in human small intestinal organoids. *P<0.05 (Unpaired t test), ***$P \leq 0.001$ (one-way ANOVA), each data point represents an independent experiment performed in duplicate.

components are combined. The signaling only occurs on the target-cell hepatocytes and not on HEK293 nor intestinal cells. Furthermore, activity depends on the presence of βKlotho binding domains on the two inactive components, as removal of βKlotho-binding ability from either the FZD or the LRP half of the molecule (or having βKlotho but not LRP binding), resulted in inactive combinations (Figs. **3** and **4**).

These results provided compelling evidence for this novel cell-targeting concept. We envision that other potential ways of dividing the WNT or WNT-mimetic molecules, including different geometries, FZD/LRP stoichiometry ratios, and linker lengths, or having one FZD- and LRP-binding arm in each component, may also result in active targeted WNT mimetics. We have termed this cell targeted WNT system, SWIFT. Our studies here focused on the WNT signaling pathway, and βKlotho/FGF21/39F7 receptor ligand system was used to illustrate the BRAID/SWIFT cell targeting concept. Whether these molecules may additional modulate endocrine FGF signaling and metabolic homeostasis could be the subject of future studies.

WNT plays important roles in many tissues during development as well as in adult tissue homeostasis and injury repair, and dysregulated WNT signaling results in various human disease conditions (Nusse and Clevers, 2017). Accordingly, SWIFT offers the opportunity to specifically target WNT activation in desired cell types, facilitating both academic research and the development of novel therapeutics.

In conclusion, we have described a novel cell-targeting approach that may be broadly applied to various signaling systems. This approach, in principle, also allows action upon a combination of different signaling pathways simultaneously, potentially providing additive or synergistic effects.

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Author contributions

HC, SJL and YP Formal analysis, Supervision, Investigation, Visualization, Methodology, Writing—review and editing; HC, SJL, RL, AS, NS, AD, YP, MV, TS, CL and YP, Resources, Investigation, Visualization, Methodology, Writing—review and editing; YL, Conceptualization, Formal analysis, Resources, Supervision, Funding acquisition, Visualization, Methodology, Writing—original draft; Writing—review and editing

Declaration of interests

All authors are current or former full-time employees and shareholders of Surrozen, Inc. YL is Executive Vice President of Research at Surrozen, Inc. A patent application is pending for the work described in this manuscript.

Materials and methods

Molecular cloning

All constructs were cloned into pcDNA3.1(+) mammalian expression vector (Thermo Fisher). The L-scFv binder was constructed by fusing the heavy-chain variable region (VH) to the N-terminus of the light-chain variable (VL) region with a 15-mer linker (GSAASGSSGGSSSGA). The anti-GFP scFv binder was constructed by fusing the VH to the N-terminus of the VL with a 15-mer-linker (GGGGSGGGGSGGGGS). All human IgG1 constructs contain the L234A/L235A/P329G mutations (LALAPG) in Fc domain to eliminate effector function (Lo et al., 2017). For generating the constructs of scFv-39F7 IgG1, the scFv binder was fused to the N-terminus of 39F7 LC with a 5-mer-linker GSGSG. To generate the construct of L-αGFP IgG1, the L-scFv was fused to the N-terminus of αGFP LC with a 15-mer-linker GSGSGGSGSGGSSGG. To generate the FGF21variant-appended F IgG molecules, FGF21 variants were fused to the C-terminus of the LC of F IgG1 (LALAPG) with a 5-mer-linker (GGSGS). FGF21FL has the mature protein sequence (H29-S209) with RGE mutations in the C-terminus (Stanislaus et al., 2017); FGF21ΔN is the sequence of FGF21FL with the deletion of the N-terminus H29–R45; FGF21ΔC is the sequence of FGF21FL with the deletion of the C-terminus S190–S209; FGF21ΔNΔC is the sequence of FGF21FL with the deletion of both the N-terminal H29–R45 and the C-terminal S190–S209.

Protein production

All recombinant proteins were produced in Expi293F cells (Thermo Fisher Scientific) by transient transfection. The proteins were first purified using CaptivA Protein A affinity resin (Repligen), unless otherwise specified. All proteins were further purified with Superdex 200 Increase 10/300 GL (GE Healthcare Life Sciences) size-exclusion chromatography (SEC) using 1x HBS buffer (20 mM HEPES pH 7.4, 150 mM NaCl). The proteins were subsequently examined by SDS-polyacrylamide electrophoresis and estimated to have >90% purity.

Super Top-Flash (STF) assays

WNT signaling activity was measured using HEK293 and Huh7 cells containing a luciferase gene controlled by a WNT-responsive promoter (STF assay) as previously reported by Zhang *et al*., 2020). In brief, cells were seeded at a density of 10,000 per well in 96-well plates. For 2-layer cell culture, either Huh7 STF or HEK293 STF cells were seeded into tissue culture-treated 6.5 mm transwell inserts (top well, Corning) with the density of 20,000. The transwell inserts were then placed into wells in a 24 well plate where HEK293 STF or Huh7 STF cells were plated with the density of 116,000 (bottom well), respectively. 24 h later, indicated WNT signaling activators were added in the presence of 3 μM IWP2 to inhibit the production of endogenous WNTs and the presence of 20 nM Fc-R-Spodin 2. Cells were lysed with Luciferase Cell Culture Lysis Reagent (Promega) and luciferase activity was measured with Luciferase Assay System (Promega) using vendor-suggested procedures.

Affinity measurement and step-binding assay

Binding kinetics of F-FGF21 series (F-FGF21FL, F-FGF21ΔN, F-FGF21ΔC, and F-FGF21ΔNΔC) to human FZD_7 CRD and βKlotho (Fisher Scientific) or L-39F7 series (L-39F7, αGFP-39F7, and L-αGFP) to human LRP6E3E4 and βKlotho, respectively, were determined by bio-layer interferometry (BLI) using an Octet Red 96 (PALL ForteBio) instrument at 30 °C and 1000 rpm with AHC biosensors (Sartorius). Various F-FGF21 or L-39F7 proteins were diluted to 50 nM in the running buffer and captured by the AHC biosensor, followed by dipping into wells containing the FZD_7 CRD, LRP6E3E4, and βKlotho at different concentrations in a running buffer or into a well with only the running buffer as a reference channel. The dissociation of the interaction was followed with the running buffer. The monovalent K_D for each binder was calculated by Octet System software, based on fitting to a 1:1 binding model.

Step-binding assays were performed with the BLI using the Octet Red 96 instrument at 30 °C and 1000 rpm with AHC biosensors. Various F-FGF21 or L-39F7 proteins were diluted to 50 nM in the running buffer and captured by the AHC biosensor, followed by dipping into wells containing the 100 nM FZD_7 CRD or 100 nM LRP6E3E4. The sensor chips next moved into 150 nM βKlothos containing 100 nM FZD_7 CRD or containing 100 nM LRP6E3E4 to check the additional bindings of β-Klotho. Sensorgram slopes were compared for βKlotho bindings.

Primary human cells

Human hepatocytes were purchased from BioIVT (10-donor pooled cryoplateable X008001-P) and cultured in LONZA hepatocyte maintenance medium (CC-3198). Briefly, plastic culture plates were coated with 20% Matrigel Matrix (CB40230C) and cells were plated in plating medium (BioIVT Z990003). After 4 h, the medium was changed to maintenance medium and refreshed every day for three days prior to the 24-h experiment.

Human small intestinal organoids were kindly supplied by the Calvin Kuo Lab at Stanford. Organoids were maintained and expanded as previously described (Sato et al., 2011). Briefly, adapted expansion medium containing advanced DMEM, 10 mM HEPES, 1x GlutaMAX, 1x penicillin–streptomycin, 1x B27, 1x N2, 1.25 mM N-acetylcysteine, 10 mM nicotinamide, 50 ng/mL recombinant human EGF, 50 ng/mL recombinant human Noggin, 20 nM R-Spondin 2, 0.1 nM L-F Wnt mimetic, 10 nM recombinant gastrin, 500 nM A83-01, and 10 μM SB202190.

Treatment of molecules was done in the presence of 20 nM R-Spondin 2 for 24 h at a concentration of 10 nM. After 24 h, the cells were harvested and RNA collected for quantitative polymerase chain reaction (qPCR). Each experiment with both primary human hepatocytes and human small intestinal organoids was repeated three times.

qPCR analysis of gene expression

RNAs from HEK293, Huh7 cells, or primary human cells were extracted using the Qiagen RNeasy Micro Kit (Qiagen). cDNA was produced using the SuperScript IV VILO cDNA Synthesis Kit (Thermo Fisher). βKlotho (*KLB*) RNA was quantified using Maxima SYBR Green qPCR master mix on a Bio-Rad CFX96 real time PCR machine.

Cycle threshold (C_t) values were normalized to the expression of constitutive *ACTINB* RNA using the following oligomers: ACTB_F1: CTGGAACGGTGAAGGTGACA. ACTB_R1: AAGGGACTTCCTGTAACAATGCA. KLB_F1: ATCTAGTGGCTTGGCATGGG. KLB_R1:CCAAACTTTCGAGTGAGCCTTG. KLB_F2:CACTGAATCTGTTCTTAAGCCCG. KLB_R2: GGCGTTCCACACGTACAGA. KLB_F3: GGAGGTGCTGAAAGCATACCT. KLB_R3: TCTCTTCAGCCAGTTTGAATGC

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Reviewer #1 (Public Review):

Summary: The goal of this study was to develop and validate novel molecules to selectively activate a cell signaling pathway, the Wnt pathway in this case, in target cells expressing a specific receptor. This was achieved through a two-component system that the authors call BRAID, where each component simultaneously binds the target cell-specific marker BKlotho and a Wnt co-receptor. These components, called SWIFT molecules, bring together the Wnt co-receptors LRP and FZD, activating the pathway specifically in cells that express BKlotho.

Results presented in the study demonstrate the desired activity of SWIFT molecules; the binding assays support simultaneous association of SWIFT with BKlotho and a Wnt co-receptor, and the Wnt reporter and qPCR assays support pathway activation in cell lines and primary cells in a BKlotho-dependent manner. In the future, the BRAID approach could be applied to activate Wnt signaling or another pathway initiated by a co-receptor complex in a cell type-specific manner, and/or in a FZD subtype-specific manner to activate distinct branches of Wnt signaling.

Strengths:

• This study successfully demonstrates a novel way to activate Wnt signaling in target cells expressing a specific marker. Given the role of the Wnt signaling pathway in key processes such as cell proliferation and tissue renewal and the value of modulating cell signaling in a cell type-specific manner, the cell targeting system developed here holds great therapeutic and research potential. It will be curious to see whether the BRAID design can be applied to other cell surface markers for Wnt activation, or for activation of other signaling pathways that require co-receptor association.

• Octet assay results show simultaneous binding of SWIFT molecules to both the Wnt co-receptor FZD/LRP and BKlotho, while negative control molecules without the FZD/LRP or BKlotho-binding module show neither receptor binding nor Wnt pathway activation. These results indicate that SWIFT molecules function through the intended mechanism.

• Exposure of two cell types simultaneously exposed to the SWIFT molecules in 2-layer cell culture demonstrated the ability of the molecules to activate Wnt signaling in a cell type- and BKlotho expression-specific manner.

Weaknesses:

• The study does not address whether the targeted cells express FGFR1c/2c/3c and whether the FGF21 full length moiety or the 39F7 IgG moiety of SWIFT molecules could unintentionally activate FGF signaling in these cells.

- https://doi.org/10.7554/eLife.90221.2.sa1

Reviewer #2 (Public Review):

Summary:

The study introduces BRAID, a novel approach for targeting drugs to specific cell types, addressing the challenges of pleiotropic drug actions. Unlike existing methods, this one involves breaking a protein drug molecule into inactive parts that are then put back together using a bridging receptor on the target cell. The individual components of this assembly are not required to be together, thereby affording it a degree of flexibility. The authors applied this idea to the WNT/-catenin signaling pathway by splitting a WNT mimic into two parts with FZD and LRP binding domains and bridging receptors. This combined method, which is called SWIFT, showed that WNT signaling was turned on in target cells, showing that cell-specific targeting is. The technique shows promise for the development of therapeutics, as it provides a way to more precisely target signaling pathways.

The authors have effectively elucidated their strategy through visually appealing diagrams, providing clear and thorough visual aids that facilitate comprehension of the concept. In addition, the authors have provided convincing evidence that the C-terminal region of FGF21 is essential for the binding process. Their meticulous and thorough presentation of experimental results emphasizes the significance of this specific binding domain and validates their findings.

Strengths:

BRAID, a novel cell targeting method, divides an active drug molecule into inactive components formed by a bridging receptor. This novel approach to cell-specific drug action may reduce systemic toxicity.

The SWIFT approach successfully targets cells in the WNT/β-catenin signaling pathway. The approach activates WNT signaling only in target cells (hepatocytes), proving its specificity.

The study indicates that the BRAID approach can target various signaling systems beyond WNT/β-catenin, indicating its versatility. Therapeutic development may benefit from this adaptability.

Weaknesses:

The study shows the SWIFT approach works in vitro using cell lines, primary human hepatocytes, and human intestinal organoids, but it lacks in vivo animal model or clinical validation. I believe future studies will determine this aspect.

The success of SWIFT depends on the presence and expression of the bridging receptor (βKlotho) on target cells. The approach may fail if the target receptor is not expressed.

- https://doi.org/10.7554/eLife.90221.2.sa0

Author Response

The following is the authors' response to the original reviews.

> ***Public Reviews:***
>
> ***Reviewer #1 (Public Review):***
>
> *Weaknesses:*
>
> *Reviewer comment: Here, the activity of SWIFT molecules was assessed in single cell types with or without BKlotho expression. Ultimately, the ability of the SWIFT molecules to activate Wnt signaling in a cell type-specific manner should be tested in the context of many different cellular identities that express BKlotho to different extents. It would be good to demonstrate that Wnt activation by SWIFT correlates with BKlotho expression level in multiple cell types - such data would strengthen the claim of cell-type specificity.*

Response: We agree with the reviewer's comment, it would be interesting to correlate the signaling level to the expression levels of βKlotho. The tools to carry out such an experiment are not currently available, as this would require a culture system that allows efficient growth of different cell types, and the reagents to detect both the receptor protein levels of βKlotho (as well as FZD/LRP) and signaling levels. We did perform an additional experiment to further support this targeting approach using a 2-layered (transwell) cell culture system. In this culture system, one cell type is put into the top well and the other cell type is put into the bottom well. Molecules to be tested were added to the media which is shared and freely diffuse across the two cell types. In this 2-layer cell system, the results again demonstrate the ability of the SWIFT molecules to specifically induce signaling only in βKlotho expressing hepatoma Huh7 cells and not in non-targeting HEK293 cells. This new data is included as Fig. 3H in the revised manuscript.

> *Reviewer comment: The study does not address whether the targeted cells express FGFR1c/2c/3c and whether the FGF21 full-length moiety or the 39F7 IgG moiety of SWIFT molecules could unintentionally activate FGF signaling in these cells.*

Response: We agree with the reviewer's comment. The receptor βKlotho and its binders (FGF21 and 39F7) were used to test the BRAID/SWIFT concept, the effects on FGF signaling were not the focus of the current study. This comment has now been added to the revised manuscript in the discussion. Inclusion of αGFP controls in the study also suggests the observed reporter activity in the targeted scenario is unlikely caused indirectly by any unexpected FGF signaling.

> ***Reviewer #2 (Public Review):***
>
> *Weaknesses:*
>
> *Reviewer comment: The study shows the SWIFT approach works in vitro using cell lines, primary human hepatocytes, and human intestinal organoids, but it lacks an in vivo animal model or clinical validation. The applicability of this approach to therapy is still unknown.*

Response: The βKlotho binder, 39F7, is specific to the human receptor and does not cross react with mouse. Unfortunately, we are not able to test these SWIFTs in a mouse model.

> *Reviewer comment: The success of SWIFT depends on the presence and expression of the bridging receptor (βKlotho) on target cells. The approach may fail if the target receptor is not expressed or available.*

Response: We agree with the reviewer, the SWIFT molecules should not induce signaling on cells where bridging receptor is not expressed, therefore, achieving target cell specificity. As pointed out by the reviewer, finding the right bridging receptor on the target cell is critical.

> ***Reviewer #1 (Recommendations For The Authors):***
>
> *Reviewer comment 1: One way to further validate the specificity of SWIFT molecules would be to apply them to a mix of different cell types and quantify BKlotho level and Wnt reporter activity at the single cell level, potentially through imaging, FACS, or transcriptomics.*

Response: We agree with the reviewer's comment, it would be interesting to correlate the signaling level to the expression levels of βKlotho. The tools to carry out such an experiment are not currently available, as this would require a culture system that allows efficient growth of different cell types, and the reagents to detect both the receptor protein levels of βKlotho (as well as FZD/LRP) and signaling levels. We did perform an additional experiment to further support this targeting approach using a 2-layered (transwell) cell culture system. In this culture system, one cell type is put into the top well and the other cell type is put into the bottom well. Molecules to be tested were added to the media which is shared and freely diffuse across the two cell types. In this 2-layer cell system, the results again demonstrate the ability of the SWIFT molecules to specifically induce signaling only in βKlotho expressing hepatoma Huh7 cells and not in non-targeting HEK293 cells. This new data is included as Fig. 3H in the revised manuscript.

> *Reviewer comment 2: The experiments presented demonstrate activation of one signaling pathway in cells specifically expressing a target receptor rather than demonstrating "the feasibility of combining different signaling pathways" as stated in the abstract.*

Response: We thank the reviewer for pointing this out and have adjusted the sentence accordingly.

> *Reviewer comment 3: What are the biological consequences of activating Wnt signaling in cells expressing BKlotho and why is that of interest? Could these biological outcomes be used as an additional, perhaps more consequential, readout for SWIFT activity?*

Response: βKlotho is expressed on several different cell types that include hepatocytes, WAT, BAT, and certain regions in CNS. Our studies here focused on the WNT signaling pathway, and βKlotho/FGF21/39F7 receptor ligand system was used to illustrate the BRAID/SWIFT cell targeting concept. Whether these molecules may additional modulate endocrine FGF signaling and metabolic homeostasis, and whether there is any interaction between βKlotho and Wnt signaling pathways could be the subject of future studies. This is now added to the revised manuscript.

> *Reviewer comment 4: The manuscript would benefit from a careful review to improve wording and address grammatical errors.*

Response: We thank the reviewer for this suggestion, and we have now had another round of language editing by a professional service.

> ***Reviewer #2 (Recommendations For The Authors):***
>
> *Reviewer comment 1. The expression of KLB in Fig 3G and 4B seems way too low and may not represent the amount on the cell surface. Did the authors validate the expression on the cell surface?*

Response: In both figures we have displayed the expression level normalized to housekeeping gene ACTB. Housekeeping genes such as ACTB can be among the most abundant transcripts in a cell. The observation that KLB mRNA detection is below ACTB mRNA levels is expected and we would argue not too low. The average real-time PCR cycle threshold (Ct) for KLB in Huh7 and primary hepatocytes was 18 and 24 respectively. To avoid any confusion, we have now displayed the expression data normalized to HEK293 and intestinal organoids as a fold difference in a new Figure 3G and 4B.

> *Comment 2. Fig 3G needs statistical significance.*

Response: We thank the reviewer for highlighting this, we have now included the statistical analysis in an updated Figure 3G.