### **Supplementary Note**

#### *Kidney-related ciliopathies*

We found that few of the NPHP-associated genes were hits in our screen, particularly for those genes mutated in NPHP only and not other ciliopathies. In particular, the NPHP genes that are associated with the Inversin compartment (*INVS*, *NPHP3*, *ANKS6*, *NEK8*) and the polycystic kidney disease genes *PKD1*, *PKD2*, and *PKHD1* are all non-hits. These genes are unlikely to be false negatives in our screen, as NPHP4 mouse mutants have been shown to have an intact Hh response1, and Inversin compartment-related ciliopathies present with kidney cysts and laterality defects but not symptoms typically linked to the Hh pathway, such as polydactyly and craniofacial abnormalities<sup>2</sup>. This finding suggests that these disorders likely arise independently of Hh signaling and possibly even involve pathomechanisms independent of cilia3.

### *Previously unrecognized ciliopathies*

The peptidyl-prolyl isomerase *Cwc27* was a hit in our screen and was recently identified as a retinitis pigmentosa (RP) gene<sup>4</sup>. Although this syndrome was not reported as a ciliopathy, the spectrum of reported *CWC27* pathologies includes canonical ciliopathy symptoms (craniofacial abnormalities, short stature, brachydactyly, and developmental delay), and we therefore suggest that *CWC27*-associated disease is a ciliopathy. Similarly, mutations in genes encoding the INTS1 and INTS8 subunits of the Integrator complex were recently described in individuals with a neurodevelopmental disorder and facial and skeletal malformations commonly seen in ciliopathies5. As the Integrator genes *Ints6* and *Ints10* are hits in our screen, disorders due to defects in Integrator complex function may also stem from altered ciliary signaling.

#### *Screen performance and CRISPR-based screening*

Several factors likely contributed to the success of our screen. Given the strong influence of cell confluence on cilium assembly and Hh signaling, the homogeneous growth conditions afforded by pooled screening were likely a major advantage. In an arrayed format, perturbations causing growth defects can indirectly affect ciliogenesis by decreasing cell density, thus generating false positives that need to be filtered out<sup>6</sup>. Pooled screens achieve confluence regardless of genotype,

and thus we can successfully identify hits that have moderate proliferation defects, including the four components of the TED complex.

Another key feature of our screen is the use of CRISPR-based gene disruption. The strong phenotypes produced by CRISPR/Cas9 likely made it possible to detect hit genes in cases where partial knockdown by RNAi or CRISPR interference (CRISPRi) might have failed to produce a detectable phenotype. A potential caveat of our approach is a decreased ability to detect hits among genes that are strictly required for cell viability. However, because ciliary signaling is dispensable for growth of cultured cells, this issue likely had a limited impact on our screen. It is also important to note that the allelic series achievable with RNAi and CRISPRi may be preferable when screening for phenotypic modifiers, as in chemical genetic or genetic interaction analyses.

The strong performance of CRISPR-based screening may also be attributable to our use of an sgRNA library comprised of many highly active sgRNAs with few off-target effects. High ontarget activity is especially important for detecting hits in dropout-based screens (in which hits become depleted) and was achieved by using 10 sgRNAs per gene and by optimizing the stability of Cas9 expression. A second benefit of using 10 sgRNAs per gene is the increased statistical power achieved when multiple effective sgRNAs are found targeting a single gene. Indeed, for hit genes such as *Dync2h1*, *Tmem107*, *Ift80*, *B9d1*, and *Grk2*, at least 7 out of 10 sgRNAs were depleted more than 4-fold (and up to 45-fold), leading to high statistical confidence. While other genes may not have been targeted as efficiently, the use of 10 elements per gene strongly increases the statistical power of hit gene detection.

An additional benefit of our screening strategy is that it readily identifies effective sgRNAs against hit genes that can be used in follow-up studies. These sgRNAs can be combined with sgRNA-resistant cDNAs to enable rigorous validation of hits and functional testing of mutant alleles, as demonstrated for the candidate disease-causing mutation in *Txndc15*. We note however that the cDNA transfection and luciferase assay readout we used for *Fam92a* and *Txndc15* may not work in all cases, such as when mutant phenotypes are mild or when over-expression of the rescue transgene interferes with function. These circumstances likely led to inconclusive results when we attempted rescue experiments for *Armc9* and *Ttc23* (data not shown). In such cases, observing concordant phenotypes for multiple independent sgRNAs provides an effective means to minimize possible off-target effects.

# *Phylogenetic analysis of TED complex genes*

Turk et al.<sup>7</sup> recently observed a phylogenetic pattern in which the presence or absence of  $\varepsilon$ -tubulin in a given species predicts whether  $\delta$ - or  $\zeta$ -tubulin is also present. The evolutionary cooccurrence of these centriolar tubulins supports a functional link between these proteins and prompted us to ask whether *Tedc1* and *Tedc2* also share a similar phylogenetic distribution. We found *Tedc1* and *Tedc2* homologs in annelids and sea urchin and *Tedc1* homologs in evolutionarily distant species such as *Paramecium tetraurelia* and *Tetrahymena thermophila* (Supplementary Table 8). Consistent with a conserved functional relationship among TED complex components, all of these species also have ε-, δ- and/or ζ- tubulins; conversely, we did not detect *Tedc1* or *Tedc2* homologs in any species lacking  $\varepsilon$ -,  $\delta$ - and  $\zeta$ - tubulins. The scope of this analysis was limited by the more rapid divergence seen for *Tedc1* and *Tedc2* sequences than for  $\varepsilon$ -,  $\delta$ - and  $\zeta$ - tubulins (Supplementary Fig. 7), but this phylogenetic distribution further supports a shared function and echoes what is seen for  $\gamma$ -tubulin and subunits of the  $\gamma$ -tubulin ring complex.

# **Supplementary Table 9. List of oligonucleotides and recombinant DNA.**





# **Supplementary Table 10. List of primary antibodies.**



# **Supplementary References**

- 1. Yee, L.E. *et al.* Conserved Genetic Interactions between Ciliopathy Complexes Cooperatively Support Ciliogenesis and Ciliary Signaling. *PLoS Genet* **11**, e1005627 (2015).
- 2. Braun, D.A. & Hildebrandt, F. Ciliopathies. *Cold Spring Harb Perspect Biol* **9**, a028191 (2017).
- 3. Chaki, M. *et al.* Exome Capture Reveals ZNF423 and CEP164 Mutations, Linking Renal Ciliopathies to DNA Damage Response Signaling. *Cell* **150**, 533-548 (2012).
- 4. Xu, M. *et al.* Mutations in the Spliceosome Component CWC27 Cause Retinal Degeneration with or without Additional Developmental Anomalies. *Am J Hum Genet* **100**, 592-604 (2017).
- 5. Oegema, R. *et al.* Human mutations in integrator complex subunits link transcriptome integrity to brain development. *PLoS Genet* **13**, e1006809 (2017).
- 6. Wheway, G. *et al.* An siRNA-based functional genomics screen for the identification of regulators of ciliogenesis and ciliopathy genes. *Nat Cell Biol* **17**, 1074-87 (2015).
- 7. Turk, E. *et al.* Zeta-Tubulin Is a Member of a Conserved Tubulin Module and Is a Component of the Centriolar Basal Foot in Multiciliated Cells. *Curr Biol* **25**, 2177-83 (2015).
- 8. Pusapati, G.V. *et al.* EFCAB7 and IQCE regulate hedgehog signaling by tethering the EVC-EVC2 complex to the base of primary cilia. *Dev Cell* **28**, 483-96 (2014).
- 9. Deans, R.M. *et al.* Parallel shRNA and CRISPR-Cas9 screens enable antiviral drug target identification. *Nat Chem Biol* **12**, 361-6 (2016).
- 10. Han, K. *et al.* Synergistic drug combinations for cancer identified in a CRISPR screen for pairwise genetic interactions. *Nat Biotechnol* **6**, 2781 (2017).
- 11. Morgens, D.W. *et al.* Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens. *Nat Commun* **8**, 15178 (2017).
- 12. Liew, G.M. *et al.* The intraflagellar transport protein IFT27 promotes BBSome exit from cilia through the GTPase ARL6/BBS3. *Dev Cell* **31**, 265-78 (2014).
- 13. Ocbina, P.J., Eggenschwiler, J.T., Moskowitz, I. & Anderson, K.V. Complex interactions between genes controlling trafficking in primary cilia. *Nat Genet* **43**, 547-53 (2011).
- 14. Dorn, K.V., Hughes, C.E. & Rohatgi, R. A Smoothened-Evc2 complex transduces the Hedgehog signal at primary cilia. *Dev Cell* **23**, 823-35 (2012).