Supplemental Figures

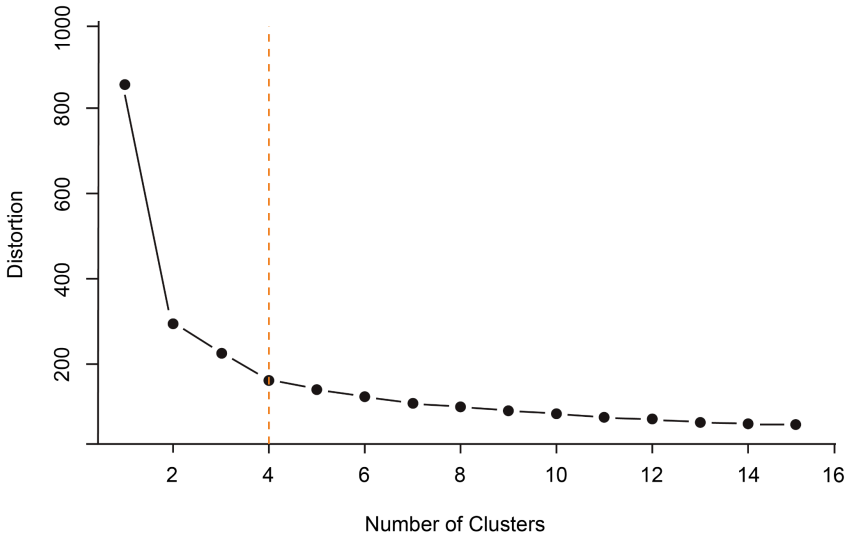

Figure S1. Elbow Plot. (A) Elbow method was used to determine the optimal clustering number for our 54 proliferation/differentiation screen genes with FDR < 0.1 and |Log2FC| ≥ 0.585 in at least 1 timepoint. We determined four to be the optimal cluster number, by identifying the inflection point of the graph (orange dotted line).

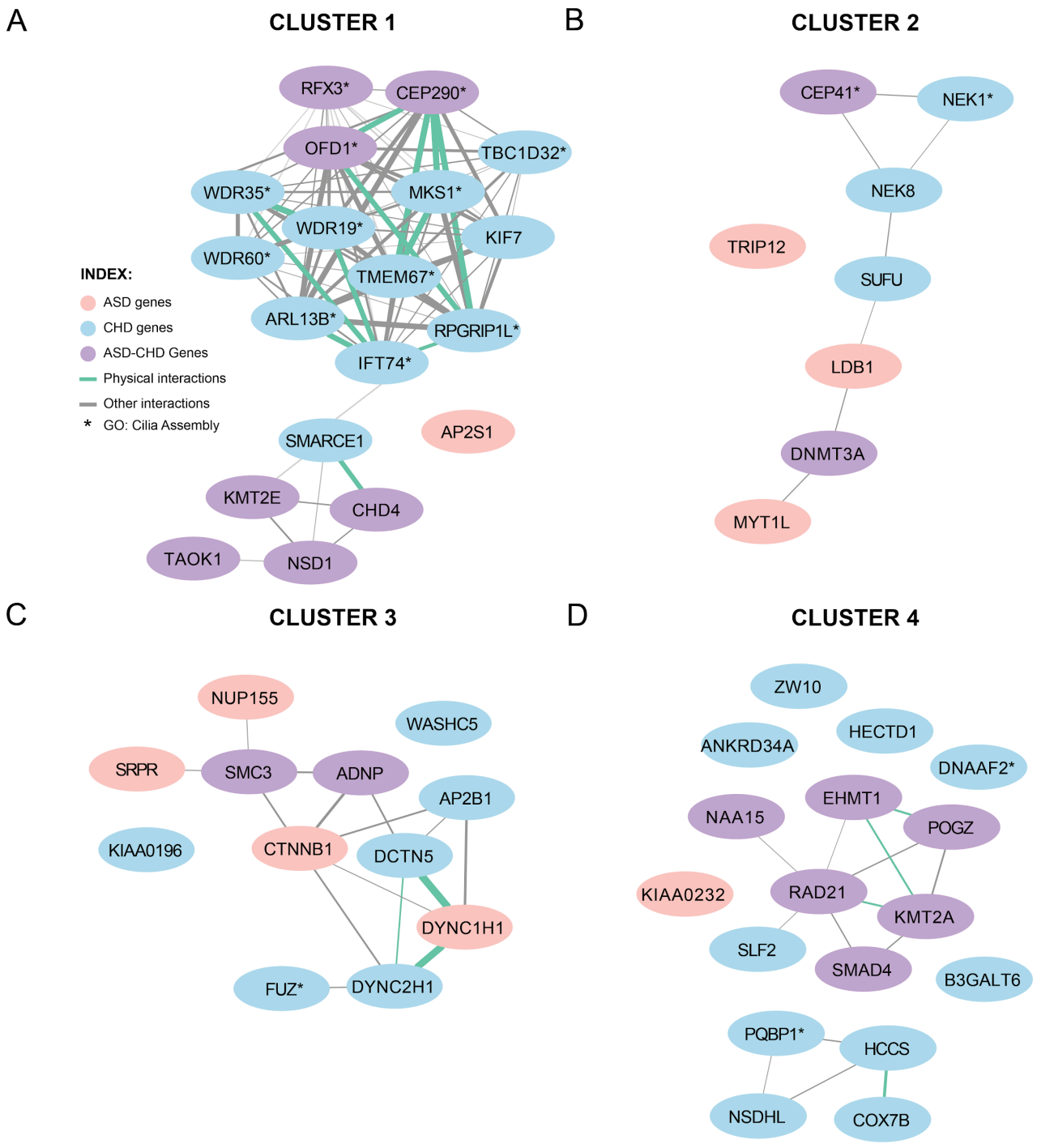

Figure S2. Cluster 1 is significantly enriched for interactions. (A-D) Visualization of Cluster 1-4 interactions identified from StringDB. ASD-genes (Satterstrom, 2019) are represented by a pink circle, CHD-genes (Jin, 2017) are represented by a blue circle, and predicted ASD-CHD genes are represented by a purple circle. Physical interactions are connected with a green line and all other types of interactions are represented by grey.

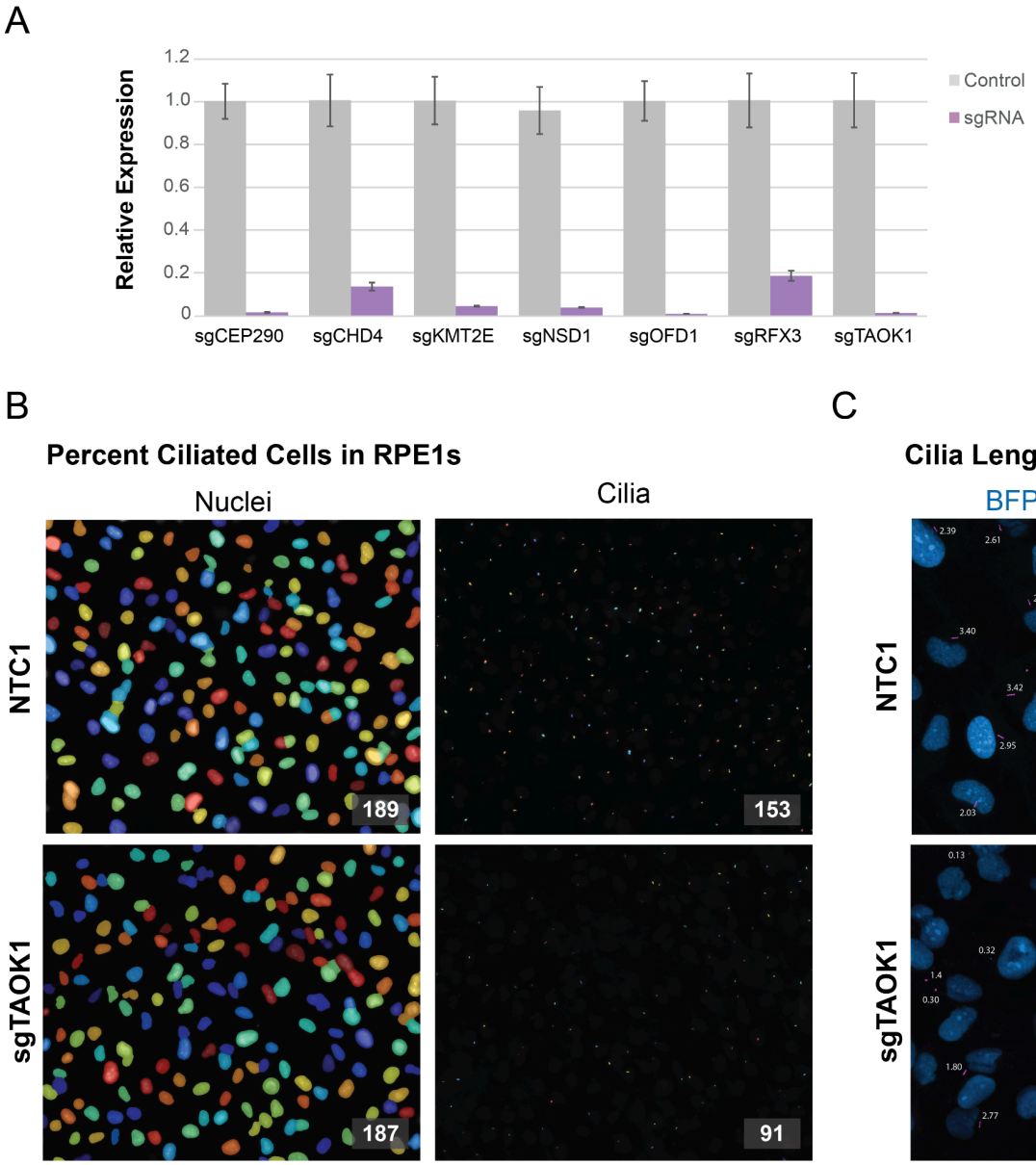

Figure S3. Cilia quantification in RPE1 cells. (A) Knockdown efficiencies of the 7 ASD-CHD gene sgRNAs were evaluated individually in established RPE1 cell lines by qPCR. (B) Representative image of percent cilia quantification of non-targeting sgRNA (NTC1; 81% ciliated) and sgTAOK1 (49% ciliated) using CellProfiler. (C) Representative image of cilia length quantification of non-targeting sgRNA (NTC1; Average length: 2.38μm) and sgTAOK1 (Average length: 0.98μm) using CiliaQ. *Image is represented as a 2D maximum projection, while cilia length was measured in 3D.

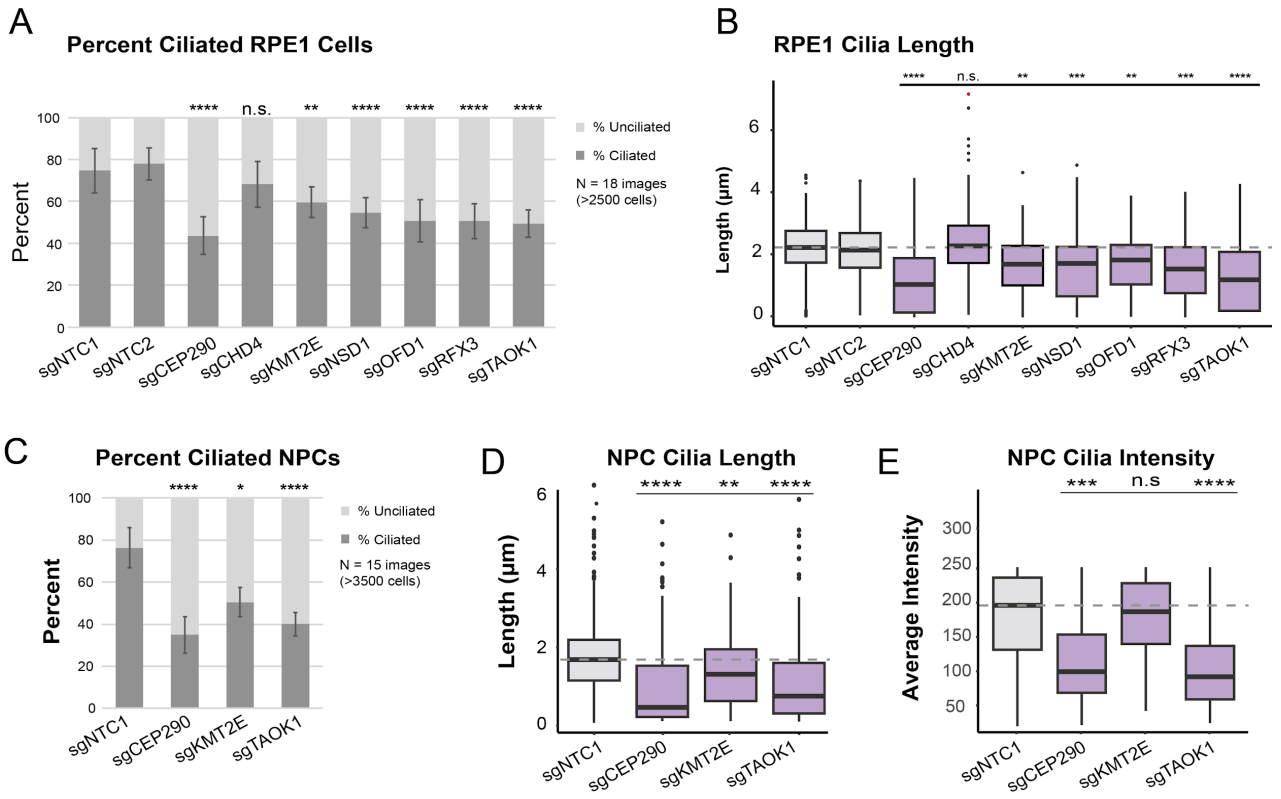

Figure S4. Knock-down of ASD-CHD genes disrupts primary cilia (without normalization) (A) We quantified percent ciliated cells in ≥2500 RPE1 cells across 18 images (3 biological replicates). (B) We captured ≥250 cells across 15 images (3 biological replicates) for quantification of cilia length (µm) in RPE1 cells. (C) We captured ≥3500 cells across 15 images (3 biological replicates) for quantification of percent ciliated cells in NPCs. (D) We captured ≥350 cells across 15 images (3 biological replicates) in NPCs. (E) Using the images from (F), we measured ARL13B intensity (a.u.) for quantification of cilia intensity in NPCs. **Significance (Dunn's multiple comparisons)*: *p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001; n.s., not significant (p > 0.05)

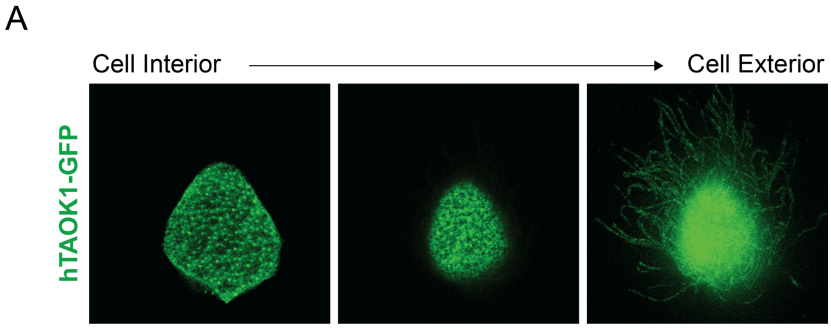

Figure S5. TAOK1 localizes to ciliary structures (A) hTAOK1-GFP injected into *X. laevis* localizes to ciliary structures of epidermal multiciliated cells. Images depict a single cell across several focal planes from cell interior to exterior. hTAOK1-GFP appears to localize to basal bodies (left), actin (middle), and ciliary axonemes (right). These images are from an animal injected only with the GFP construct (so as not to have potential crosstalk from fluorescence channels from co-stains, but similar results were observed with costains for basal bodies and axonemes).

Supplemental Tables

Table S1 - List of screened genes (Log2FC, PVal, ASD-satterstrom, CHD-Jin, ASD-CHD Rosenthal, ASD-CHD Genetic, CHD-SFARI)

Table S2 - List of significant genes input for k-means clustering (per replicate, Cluster number, Log2FC, PVal, Category (ASD, CHD, ASD-CHD))
*Legend: Dx = day number; Rx = replicate number

Table S3 - ToppGene Enrichments (Biological Process and Cellular Component) of Cluster 1 genes with CRISPRi screen genes used as background correction (Tab 1 - CRISPRi BG), as well as, default background correction (Tab 2 - Default BG)