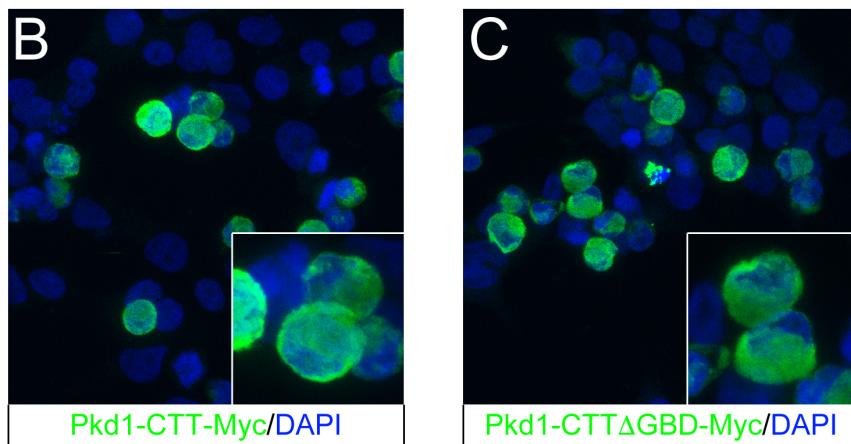
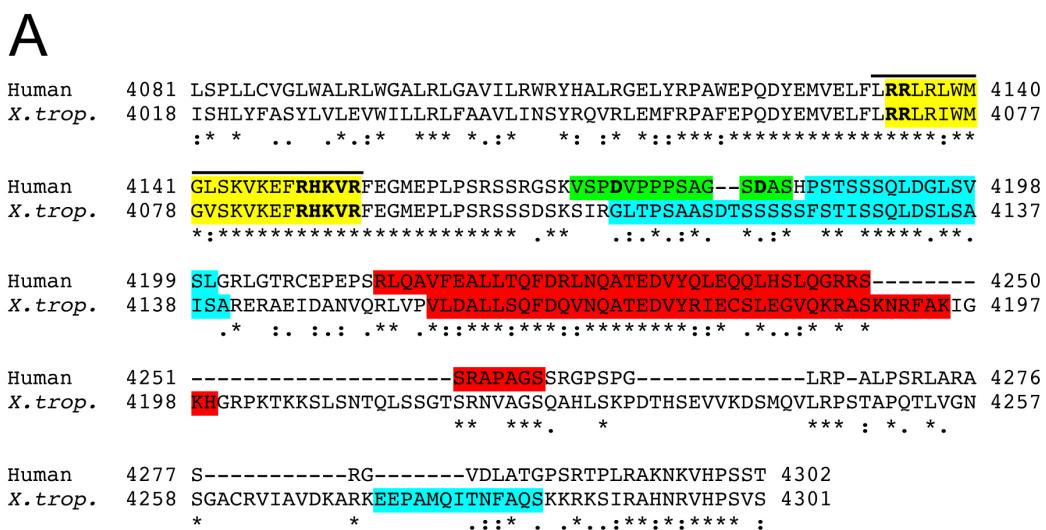
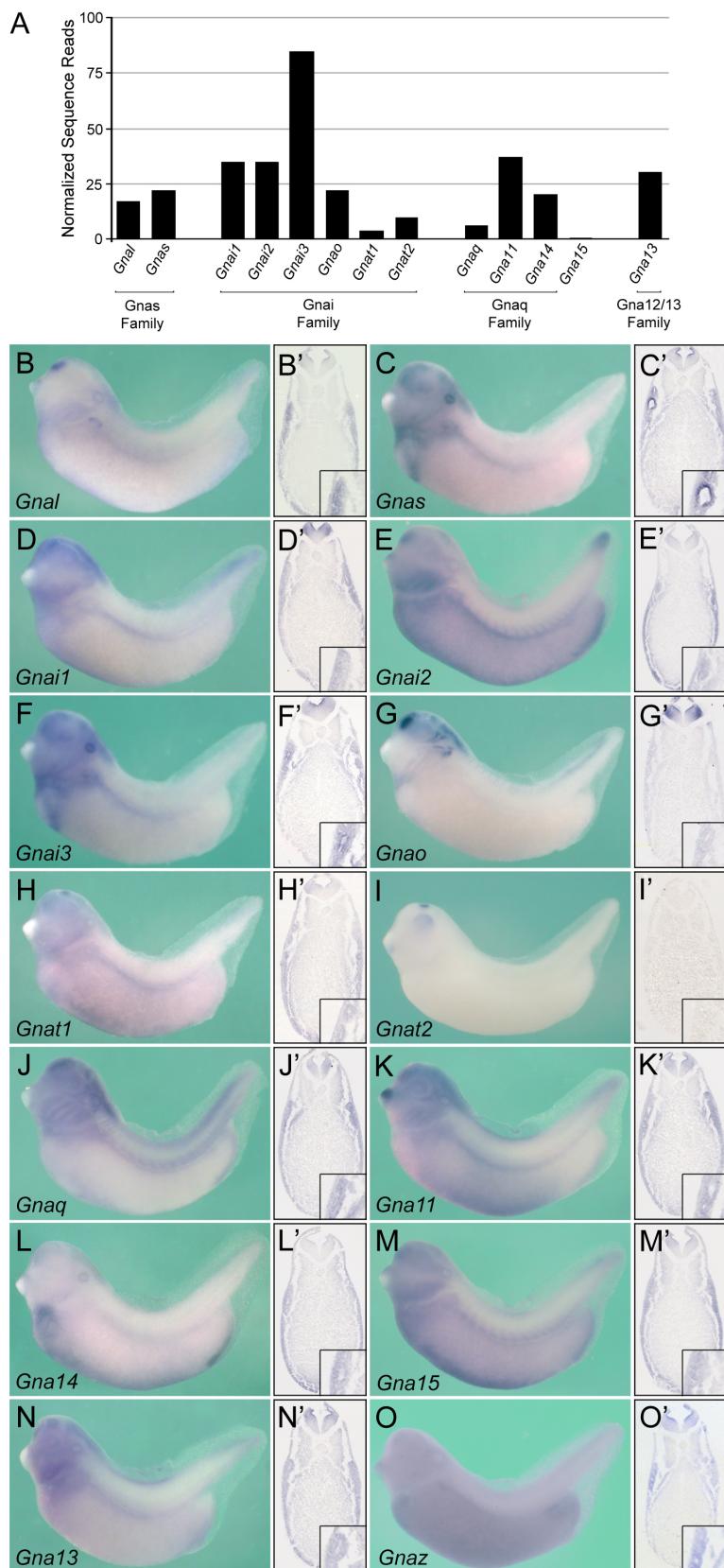


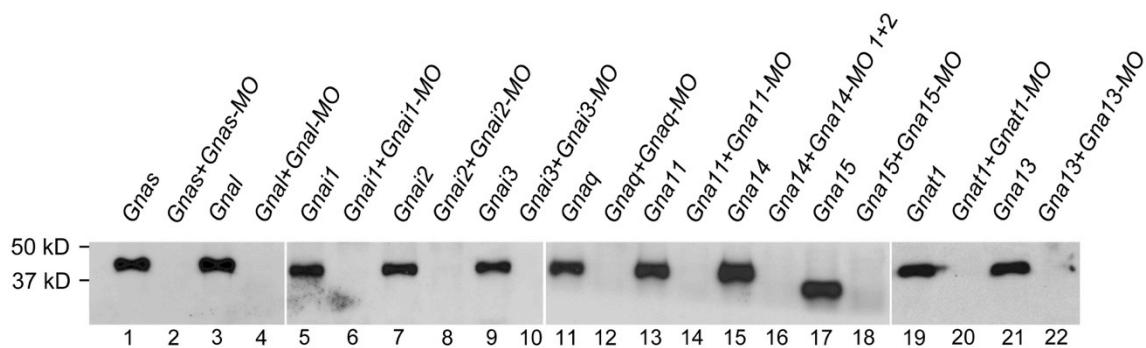
**Figure S1: Expression of Proximal-Distal Marker Genes in *Gnas* Morphants.** Whole mount *in situ* hybridization of uninjected control and *Gnas*-MO-injected embryos at stage 39 with *Nphs1* (A,B), *Sglt1K* (C,D), *Nkcc2* (E,F), *Ncc* (G,H) and  $\beta 1\text{-Na/K-ATPase}$  (I,J).



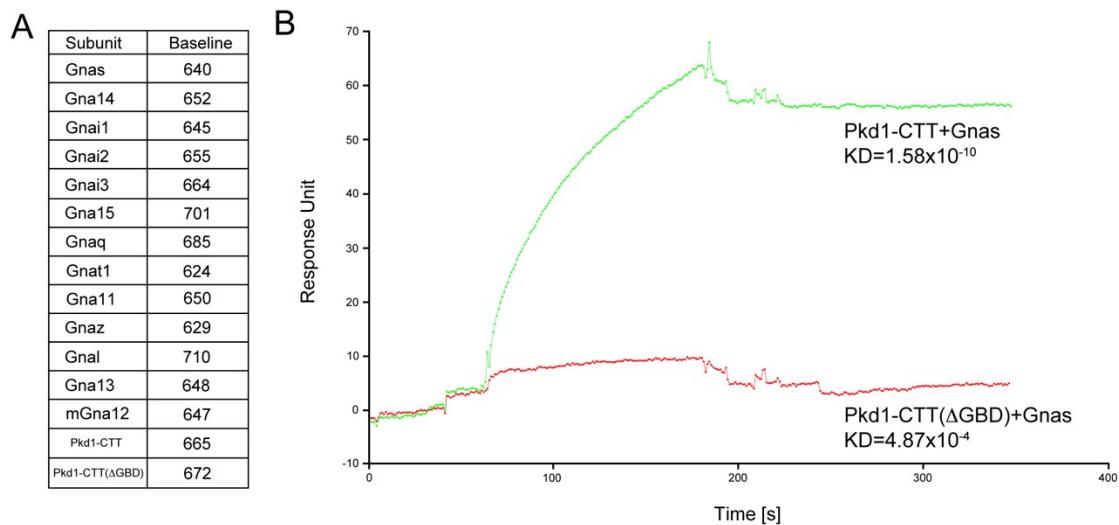
**Figure S2: Conservation of the C-terminal Tail of Pkd1.** (A) ClustalW alignment of the intracellular domain of Polycystin-1 protein from human (GenBank Accession #NP\_000287.3) and *Xenopus tropicalis* (GenBank Accession #XP\_002932517.1). Four previously described domains were analyzed. The G-protein binding signature (GBD) is based on the analysis by Parnell et al. (1998). It is indicated in yellow and the domain-identifying amino acids (BB....BBxxB) are bolded. This sequence overlaps with the Nuclear Localization Sequence (NLS) described in Chauvet et al. (2004) and is indicated by a black line above the human sequence. The PEST sequences were identified using *epestfind*. The optimal and predicted domains are indicated in green and turquoise, respectively; the key amino acids identified in Low et al. (2006) are indicated in bold. The coiled-coil domain were identified using *Paircoil2* and are labeled in red. (B,C) Immunofluorescence analysis of HEK293T cells transiently transfected with Pkd1-CTT-Myc (B) or Pkd1-CTT $\Delta$ GBD-Myc (C). Nuclei were counterstained with DAPI (blue). Insets show close-up of individual cells.



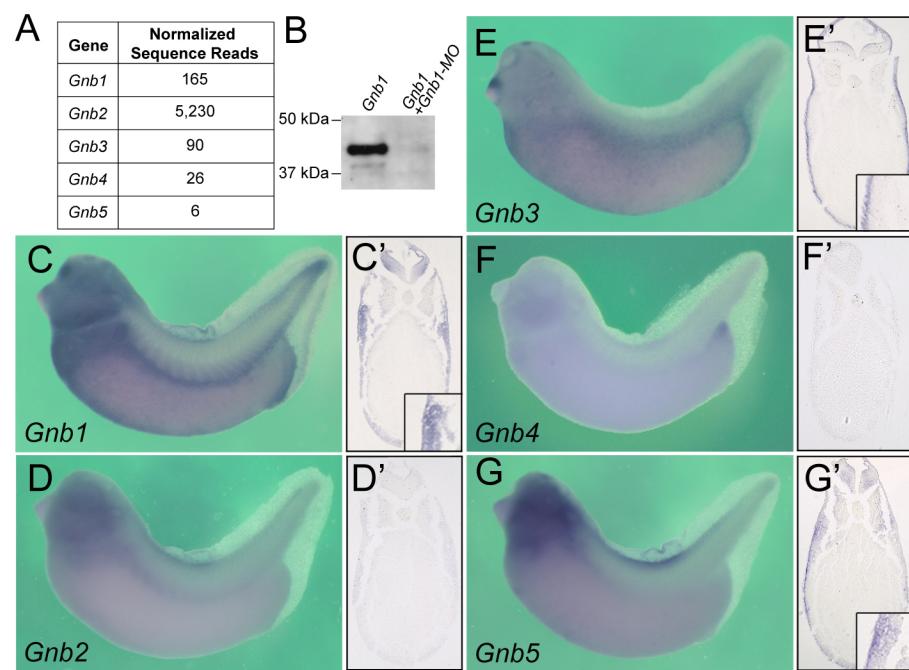
**Figure S3: Expression of G-Protein Alpha Subunits in *Xenopus* Embryos.** (A) Quantification of the expression levels of G-protein alpha subunits of stage 39 *Xenopus tropicalis* embryos using RNAseq. (B–O') Whole mount *in situ* hybridization of *Xenopus laevis* embryos and paraplast sections thereof demonstrating the expression of G-protein alpha subunits in stage 35 embryos. Insets show close-ups of the pronephric kidney. Note that only *Gnao* (G,G') and *Gnat2* (I,I') are not expressed in the pronephric kidney.



**Figure S4: Knockdown of Different G-Protein Alpha Subunits.** Analysis of MO knockdown efficacy by *in vitro* transcription/translation.



**Figure S5: SPR Analysis of the Interaction Between Pkd1 and G-Protein Alpha Subunits.** (A) Baseline demonstrating that all the *in vitro* transcribed/translated G-protein alpha subunits were bound to the streptavidin chip in comparable amounts. (B) Representative sensorgram showing the strong interaction of Gnas with a GST-Pkd1-CTT fusion protein, but not with the GST-Pkd1-CTT $\Delta$ GBD. The equilibrium dissociation constants ( $K_D$ ) for both interactions are shown.



**Figure S6: Expression Analysis of G-Protein Beta Subunits.** (A) Quantification of the expression levels of G-protein beta subunits of stage 39 *Xenopus tropicalis* embryos using RNAseq. (B) Analysis of *Gnb1*-MO knockdown efficacy by *in vitro* transcription/translation. (C-G') Whole mount *in situ* hybridization of *Xenopus laevis* embryos and paraplast sections thereof demonstrating the expression of G-protein beta subunits in stage 35 embryos. Insets show close-ups of the pronephric kidney. The expression of *Gnb1* in the pronephric kidney was the most pronounced of all the G-Protein beta subunits and was, thus, selected for the knockdown studies.

**Table S1: Summary of the Plasmids and MOs.*****Antisense Probes for in situ hybridization***

<b>Gene</b>	<b>Clone ID</b>	<b>Vector</b>	<b>Antisense</b>	<b>Sense</b>
<i>gnal.S</i>	8317937	pExpress1	T7/EcoRI	Sp6/NotI
<i>gnas.L</i>	6864835	pCMVsport6	T7/Asp718	Sp6/NotI
<i>gnai1.S</i>	8543262	pCS111	T7/PstI	Sp6/NotI
<i>gnai2.S</i>	3404925	pCMVsport6	T7/EcoRI	Sp6/NotI
<i>gnai3.S</i>	8820619	pCS111	T7/PstI	Sp6/NotI
<i>gnao1.L</i>	6947982	pCMVsport6	T7/BamHI	Sp6/NotI
<i>gnat1.L</i>	6950310	pCMVsport6.ccdb	T7/Clal	Sp6/Apal
<i>gnat2 (*)</i>	7018744	pCMVsport6	T7/EcoRI	Sp6/NotI
<i>gnaz.S</i>	amplified by PCR	PGEM T-easy	Sp6/NotI	T7/Sall
<i>gnaq.L</i>	8074729	pCS111	T7/EcoRV	Sp6/Xhol
<i>gna11.S</i>	3404901	pCMVsport6	T7/KpnI	Sp6/NotI
<i>gna14.S</i>	5162325	pT7T3D-Pacl	T3/Xhol	T7/NotI
<i>gna15.L</i>	8542421	pCS111	T7/Clal	Sp6/Xhol
<i>gna13.S</i>	6870976	PBlueSk-	T3/KpnI	T7/NotI
<i>gnb1.S</i>	8074931	pExpress1	T7/EcoRV	Sp6/Xhol
<i>gnb2 (*)</i>	7201226	pCMVsport6	T7/Sall	Sp6/NotI
<i>gnb3.S</i>	5571340	pCMVsport6	T7/Sall	Sp6/NotI
<i>gnb4.L</i>	3743760	PBlueSk-	T3/EcoRV	T7/NotI
<i>gnb5.L</i>	6955985	pCMVsport6.ccdb	T7/EcoRV	Sp6/Xhol

(\*) genomic sequence information too incomplete to distinguish between S and L.

***Antisense Morpholino Oligomers***

<b>Gene targeted</b>	<b>MO sequences</b>	<b>Abbreviation</b>
<i>gnal.S + gnal.L</i>	5'-CCT AAA CAA CCC ATA TTA ATG GTC C-3'	<i>Gnal-MO</i>
<i>gnas.S + gnas.L</i>	5'-AGA CAC CCC ATG GTC CGT GTG GGC T-3'	<i>Gnas-MO</i>
<i>gnai1.S + gna1.L</i>	5'-CTT CGG CGC TCA GAG TAC ATC CCA T-3'	<i>Gnai1-MO</i>
<i>gnai2.S + gna2.L</i>	5'-CAG CGA TAT GTC GCG ACA CAG CCC C-3'	<i>Gnai2-MO</i>
<i>gnai3.S + gna3.L</i>	5'-CCT CGG CAC TCA ATG TGC AGC CCA T-3'	<i>Gnai3-MO</i>
<i>gnat1.S + gnat1.L</i>	5'-AGC ACT GGC TCC AGC CCC CAT ATT C-3'	<i>Gnat1-MO</i>
<i>gnaq.S + gnaq.L</i>	5'-ACG CCA TGA TGG ACT CCA GAG TCA T-3'	<i>Gnaq-MO</i>
<i>gna11.S + gna11.L</i>	5'-TTG AAT CTA GAG TCA TCC CTT CCC C-3'	<i>Gna11-MO</i>
<i>gna14.S</i>	5'-GCA GTT GCT GAG TGC GAC CCC TCG C-3'	<i>Gna14-MO1</i>
<i>gna14.L</i>	5'-CAA CCC GCC ATG CCC AAG CGC AAT T-3'	<i>Gna14-MO2</i>
<i>gna15.S + gna15.L</i>	5'-CAA GGC ATC TTG TAG TAC CAG GTA C-3'	<i>Gna15-MO</i>
<i>gna13.S + gna13.L</i>	5'-CAG GAA GTC CGC CAT CTT ACA CAC T-3'	<i>Gna13-MO</i>
<i>gnb1.S + gnb1.L</i>	5'-GGC GTA GCT GAT CTA GTT CAC TCA T-3'	<i>Gnb1-MO</i>
<i>pkd1.S + pkd1.L</i>	5'-TCC TTA TGG TCC GAG TTA CCT TGG G-3'	<i>Pkd1-sMO</i>
<i>pkd2.S + pkd2.L</i>	5'-GGT TTG ATT CTG CTG GGA TTC ATC G-3'	<i>Pkd2-MO</i>
<i>rapgef4.S rapgef4.L</i>	5'-CTT GGC GAA ATC CCA TTA CCT CTG T-3'	<i>Rapgef4-MO</i>