Figure S1 Retinal cell differentiation appears largely normal in *snw* embryos. (A-D) *snw* embryos at 5 dpf show typical expression of various retinal cell markers (blue) throughout the retina; images are counterstained with the nuclear stain, Sytox (green). (A) Ganglion cells were stained with the Zn8 antibody, (B) rod cells were stained with anti-Zpr3, (C) bipolar cells were stained with anti-PKC, and (D) cone cells were stained with anti-Zpr1.

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A

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MIPVVPVESC  THVLAEFDCL  DPLLSALRLD  SGRIKCTCLS  VSRKWLALGT  SAGGLHLIQR  DGWKQKLILT  HKEGSITQVS   80
CCPHDEDFIA  VATSQGLVVV  WELHLERRGR  PERASVSWEH  RGVTVTSLCW  DTVALRVFAG  DVGGKVSCVR  AGSSKLGKGS  160
AFVIFPVQTV  TTVDSRVVQL  GYTDGHLVIS  SLSRCYLCDT  EREKFWRVGN  KERDGEFGAC  FLTQGLAGQR  GQLVGCPAPL  240
LFCARPGSRI  WEASFSGEVL  STHQFKQLLA  VPPLPLVSCK  NEPHFNPTQT  NPQSLAFPRL  LQFGDQNLLT  WTDSAIYIFT  320
PHSGQVLLWT  EVKDVLEISV  FRNDLFCLHG  DGRLSHMSLV  SPDRCVERLM  KRENWTIAAT  VCCMFQHAIT  TSKARKSLSI  400
DRLEHLKAQL  NSTSHQQLIG  QLEEVISKLE  PLDSACSSRR  SSISSHESFN  VLDCGIYRVI  SRRGSQSDDD  ASSLANQSML  480
EDERLKEFSF  TEEEQVDNDS  ASVRGEGDRS  DLGLQFLPLP  FRSKPPRVAL  QAVRDSVSSF  MKKTTEKINT  LQMNADLWPR  560
PDLREGVQGE  VASTASPISE  ESEQELNTEH  SGSESELLEL  RAATKKAISQ  IQDPMVLLDP  LCLSDVLQEW  APVLERALGP  640
EDQILPVETT  NPEEKTLEEE  ELVSSMSCCV  VVQPEISTSP  AADPDESATH  TEEEDFREST  PCSIAPVRAQ  FPPLANHVEL  720
IQLFSPKPLP  PDLQADLSLL  ACLYLEMGCP  GRGGMESVCV  FLRRFFFLLD  QERVRRMCML  RYRENREVLK  AYIAGMLEFT  800
QASKVVEVIQ  KGDLLKSLRS  LRELQPWNAP  LLLSHLYRLY  EKHGEVAVRA  YPQFYPTILP  SDIMAMALPS  HFLPYLDNLV  880
QSRAEQQRLS  FLGSLLQPET  LRQDWLELAL  SHDAPQREDT  LTHDGQPRWH  SHFFSWGYGR  LLSLLIRLPA  DLASKQKMLD  960
MCKAHGYWMG  YLYLCRELQR  RAEAFSAICR  LDDMTLLEGD  DGIVPQSLDE  WVLLLQLSQQ  ISASDESSLT  STKNSNGSCL  1040
VDANSNGDCS  SGLSNGSTDW  SIQVSPENII  LRLVRVFGPD  RALTALQEHG  IPVDHSSRST  LVCDLLRMAE  KRQRALIQSM  1120
LERCDRFLWS  QHA*                                                                                1133
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B

Amino acid change	Residue change
76, I->N	227, ATC -> AAC
107, R->H	320, CGC -> CAC
133, V->A	398, GTG -> GCG
170, V->I	508, GTC -> ATC
182, Y->N	544, TAC -> AAC
555, A->S	1663, GCT -> TCT
1025, D->G	3074, GAT -> GGT
1034, N->S	3101, AAC -> AGC
1035, S->T	3104, AGC -> ACC
1062, I->L	3184, ATT -> CTT
1063, Q->R	3188, CAG -> CGG

Figure S2 *Danio rerio hps5* **sequence**. (A) *hps5* was cloned from both wild-type and *snw* embryos and aligned for comparison. Eleven single nucleotide polymorphisms (SNPs) were detected in the *snw* sequence when compared to the predicted Hps5 Zv9 sequence, highlighted by pink squares. Ten of these SNPs were eliminated as being the causative *snw* mutation as they were detected in wild-type AB strain adult zebrafish. (B) The amino acid sequence changes and corresponding nucleotide sequence changes are given, along with position numbers for reference.
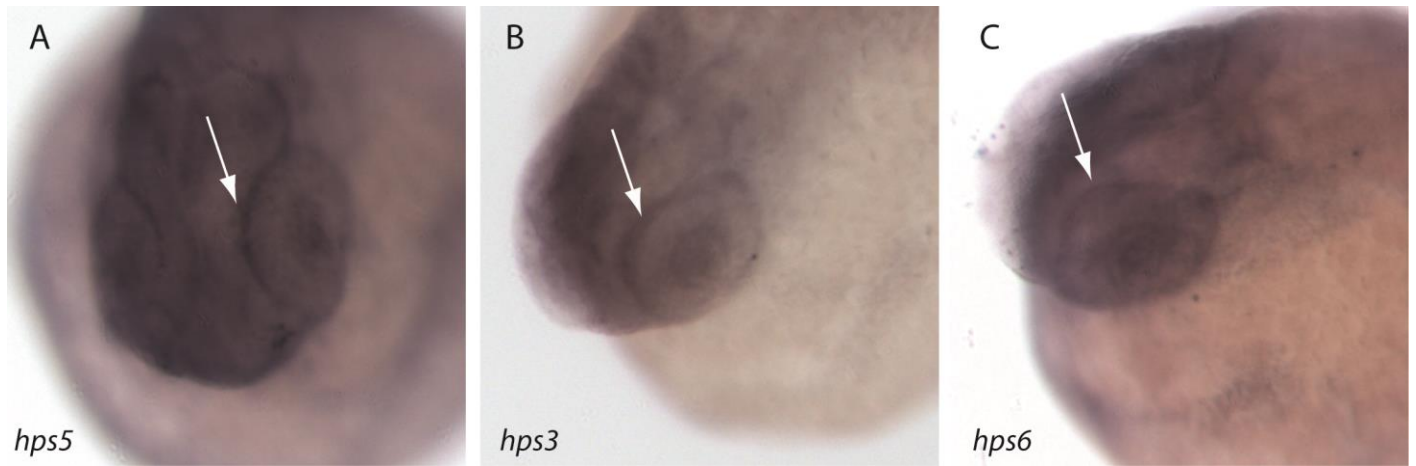
Figure S3   Bloc2 complex members are expressed in the developing zebrafish eye. *in situ* hybridization in 26hpf wild-type zebrafish embryos demonstrates that (A) *hps5*, (B) *hps3*, and (C) *hps6* are all expressed in the developing zebrafish embryo. The retinal pigmented epithelial (RPE) cell layer is identified by white arrows. Sense controls showed non-specific, background stain.
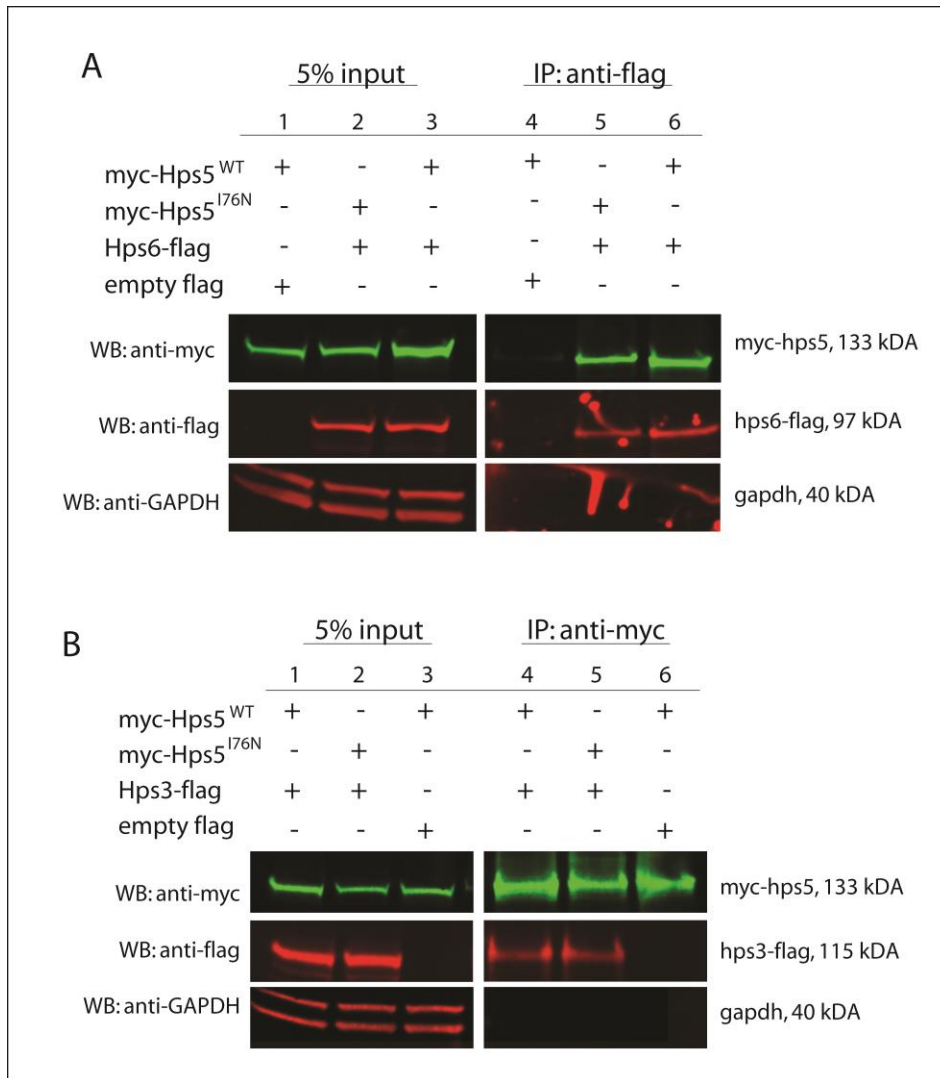
Figure S4 Both Hps5^WT and Hps5^I76N bind to Hps6 and Hps3 *in vitro*. (A) COS7 cells were transiently co-transfected with Hps5^WT/empty vector, Hps5^I76N/Hps6, or Hps5^WT/Hps6 (lanes 1, 2, 3). Whole cell lysates were subjected to co-immunoprecipitation with flag antisera (IP:anti-flag, lanes 4, 5, 6). Western blots were detected with the antibodies indicated to the left (WB). Hps6 co-precipitates both Hps5^WT and Hps5^I76N individually (lanes 5, 6). (B) COS7 cells were transiently co-transfected with Hps5^WT/Hps3, Hps5^I76N/Hps3, or Hps5^WT/empty vector (lanes 1, 2, 3). Whole cell lysates were subjected to co-immunoprecipitation with anti-myc antisera (IP:anti-myc, lanes 4, 5, 6). Western blots were detected with the antibodies indicated to the left (WB). Both Hps5^WT and Hps5^I76N co-precipitate Hps3 (lanes 4, 5).

Table S1   Hps5^WT protein modeling parameters from SwissModel of entire protein (residues #1-1133)

Residues	Sequence identity	E-score	Q-MEAN4 raw score	Q-MEAN4 Z-score	ANOLEA score at #76	GROMOS score at #76
31-152	22.0%	2.0E-7	0.480	-3.34	~ +1	~ +20
73-189	17.4%	2.7E-6	0.407	-3.89	~ +4	~ +10
31-358	12.6%	1.4E-6	0.208	-8.99	~ +130	~ +10

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Table S2   Hps5WT protein modeling parameters from SwissModel of N-terminus (residues #1-370).

Residues	Sequence identity	E-score	Q-MEAN4 raw score	Q-MEAN4 Z-score	ANOLEA score at #76	GROMOS score at #76
30-103	21.6%	4.6E-19	0.667	-0.736	-5	+10

Table S3   Hps5I76N protein modeling parameters from SwissModel of entire protein (residues #1-1133)

Residues	Sequence identity	E-score	Q-MEAN4 raw score	Q-MEAN4 Z-score	ANOLEA score at #76	GROMOS score at #76
31-152	22.0%	1.9E-7	0.478	-3.36	~ -3	~ -180
73-189	17.4%	2.6E-6	0.418	-3.78	~ +2	~ -150
30-358	14.5%	3.2E-6	0.284	-7.82	~ +4	~ -40

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Table S4 Hps5I76N protein modeling parameters from SwissModel of N-terminus (residues #1-370).

Residues	Sequence identity	E-score	Q-MEAN4 raw score	Q-MEAN4 Z-score	ANOLEA score at #76	GROMOS score at #76
30 to 104	19.5%	3.2E-24	0.584	-1.27	~ -2.5	~ -160