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.