Supplemental Information

Supplemental Fig.1. dbx1a, her4.2, nxph1, hes5 and plxnd1 relative expression values (Efficiency based method; Pfaffl, 2001) were plotted in a 3D graph for both groups (WT sib and mib mutants). Note a co-variation pattern of expression of these genes; in this example, when dbx1a was plotted against her4.2 and nxph1 its expression decreased (represented by green color) simultaneously with the increase of her4.2 and nxph1 expression (red color) in the 3 dpf WT siblings (A). In mib mutants, we observe an opposite pattern, dbx1a expression increases (red) with down-regulation of her4.2 and nxph1 (green) (B). A similar pattern is shown when dbx1a was plotted against hes5 and plxnd1 in WT sib (C) and mib mutants (D); dbx1a is inversely correlated with Hes5. Abbreviations: *dbx1a*, developing brain homeobox 1a; *her4.2*, hairy-related 4.2; *hes5*, hairy and enhancer of split 5; *nxph1*, neurexophilin 1 and *plxnd1*, plexin D1.

Supplemental Table 1. Pearson correlation coefficients are summarized in this table. The highest correlation coefficients >0.70 or < -0.70 significant at the 0.01 level are indicated by two asterisks and the correlation coefficients < 0.7 or >-0.7 significant at the 0.05 level are indicated by one asterisk.

Supplemental Table 2. Primer's sequences, GeneBank accession number and amplicon size for the investigated genes in conventional RT-PCR; primers indicated by asterisks were also used in preparing the probes for In Situ Hybridization DNA (template preparation using PCR amplification).

Supplemental Table 3. Real-time qPCR primer sequences and amplicon sizes for the SybrGreen assays.

Supplemental Table 4. qPCR efficiencies for all the gene of interest, slope of the curves, intercept and the correlation coefficient were estimated using the equation E=10[-1/slope] (qCalculator software). Cycle threshold (CT) values were obtained by the standards serial dilutions assayed in triplicate (4-fold serial dilution).