Zebrafish complement factor H and its related genes: identification, evolution and expression

Functional & Integrative Genomics

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Supplementary Fig. S2 Alignment of SCRss and SCRLs of zebrafish CFH and CFHLs using the
MegAlign program (DNASTAR) by the Clustal W method. Shaded (with solid black) residues are the
amino acids that match the consensus. Gaps introduced into sequences to optimize alignment are represented by (-)