Microarray quality assessment

Figure S1. Distribution analysis of hybridization success across 14 microarray experiments. For each probe, the number of times it was called “present” by Agilent Feature Extraction 9.5.1 software was calculated. On the y-axis, the number of positive calls in 14 experiments (0 corresponds to probes that never hybridized, 14 corresponds to probes that always successfully hybridized). On the x-axis is the number of probes falling into each group (0-14). The exact count of probes and the corresponding percentage are also reported for each group.

Figure S2. Correlation between levels of gene expression measured by Probe_1 and Probe_2. Each plot describes the distribution of observed fold-changes between Probe_1 and Probe_2 for each array experiment in 38 days-old sea bass heads. On the y-axis are the Fold-change (expression values ratio between Probe_1 and Probe_2) distributions calculated for each biological replicate of Stage 38 (x-axis).