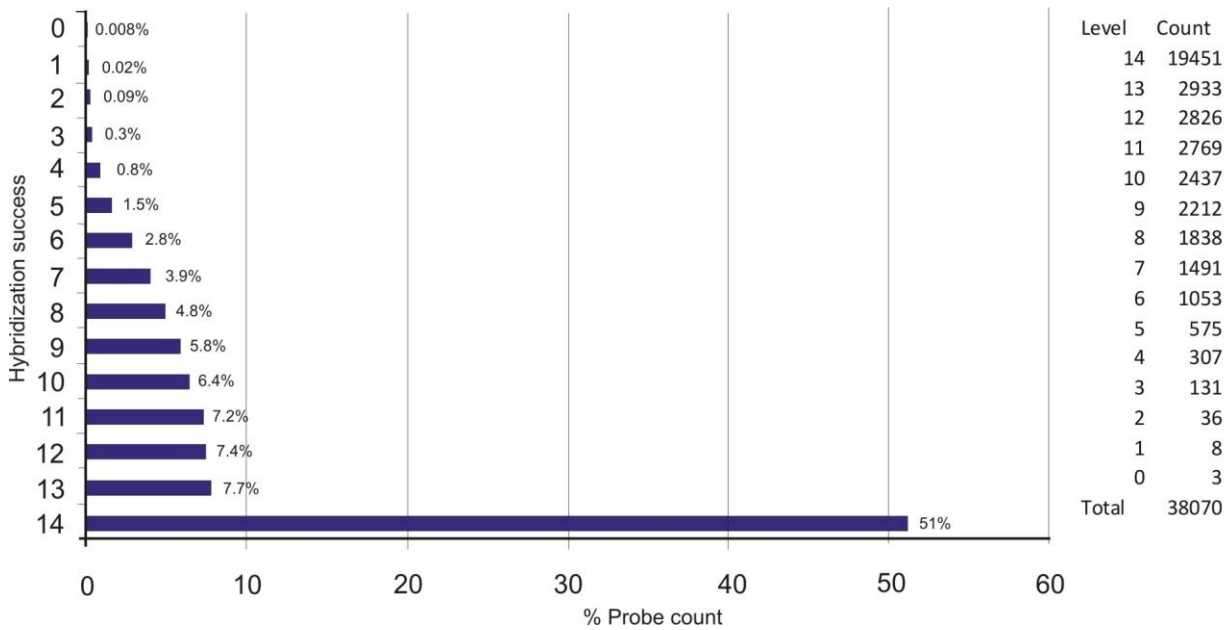
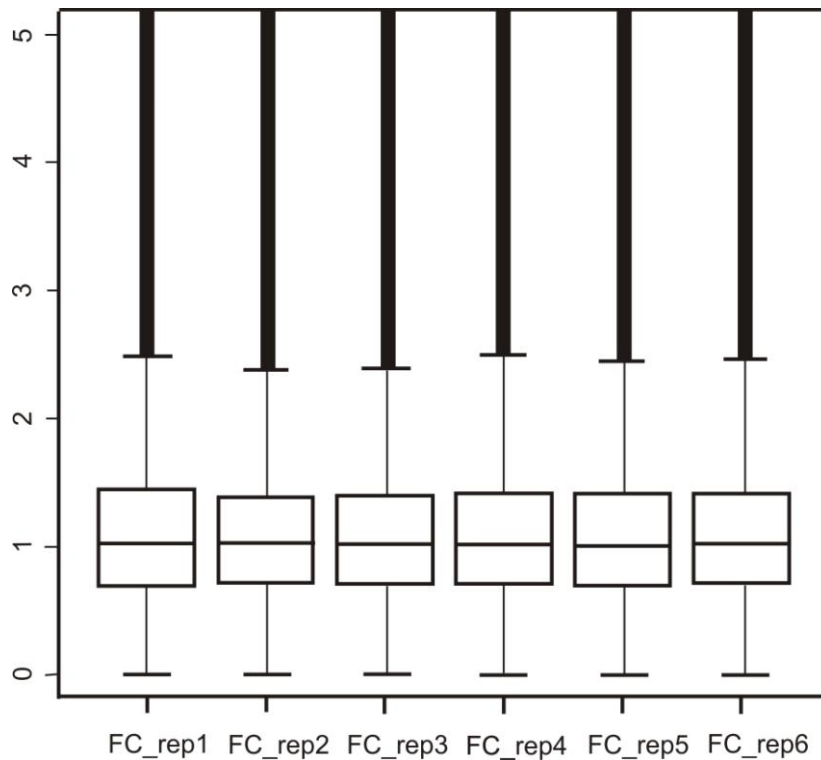


### Microarray quality assessment



**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).