**Table S4 iHS analysis.** Numbers of SNPs showing evidence of recent positive selection in regions with different levels of evolutionary conservation versus those expected at random. Expected values, their standard deviations and p-values were estimated from permutation tests.

| Type | Observed | Expected | Standard deviation (+/- ) | Fold change | Direction of difference | P |
|---|---|---|---|---|---|---|
| Non-conserved | 87 | 60 | 7 | 1.45 | Enriched | <0.005 |
| At least 1 other teleost | 105 | 131 | 7 | 0.80 | Depleted | <0.005 |
| At least 2 other teleosts | 95 | 110 | 7 | 0.86 | " | 0.014 |
| At least 3 other teleosts | 72 | 89 | 7 | 0.81 | " | 0.008 |
| Four other teleosts | 38 | 27 | 5 | 1.41 | Enriched | 0.032 |

Numbers of SNPs showing evidence of recent positive selection in regions with different levels of evolutionary conservation versus those expected at random. Expected values, their standard deviations and p-values were estimated from permutation tests.