

Table S5. Maximum likelihood analysis of a Kingman-coalescent HKA test of neutrality and selection at three genes in Atlantic cod.

| Description | $\ln L$ | T | Test | df | <i>Hbα2</i> | | <i>Myg</i> | | <i>Ckma</i> | |
|--------------------------|---------|------|------|------|-------------------------------|-----|------------|-----|-------------|------|
| | | | | | θ | k | θ | k | θ | k |
| Neutral, all $k = 1$ | -18.66 | 2.46 | | | 0.0035 | 1 | 0.0068 | 1 | 0.0056 | 1 |
| Selection at <i>Ckma</i> | -17.47 | 3.86 | 2.38 | 1 | 0.0029 | 1 | 0.0054 | 1 | 0.0032 | 2.12 |

Test is twice the $\ln L$ difference of the two models, neutrality and selection at *Ckma*. Three loci are under test: Hemoglobin α 2 (*Hb α 2*), Myoglobin (*Myg*), and Creatine Kinase Muscle (*Ckma*). θ is the scaled effective population size and the parameter k measures changes in diversity due to selection. Based on method of Wright and Charlesworth (2004).