Next-generation sequencing and the collection of genome-wide data allow identifying adaptive variation and footprints of directional selection. Using a large SNP data set from 259 RAD-sequenced European eel individuals (glass eels) from eight locations between 34 and 64°N, we examined the patterns of genome-wide genetic diversity across locations. We tested for local selection by searching for increased population differentiation using FST-based outlier tests and by testing for significant associations between allele frequencies and environmental variables. The overall low genetic differentiation found (FST = 0.0007) indicates that most of the genome is homogenized by gene flow, providing further evidence for genomic panmixia in the European eel. The lack of genetic substructuring was consistent at both nuclear and mitochondrial SNPs. Using an extensive number of diagnostic SNPs, results showed a low occurrence of hybrids between European and American eel, mainly limited to Iceland (5.9%), although individuals with signatures of introgression several generations back in time were found in mainland Europe. Despite panmixia, a small set of SNPs showed high genetic differentiation consistent with single-generation signatures of spatially varying selection acting on glass eels. After screening 50 354 SNPs, a total of 754 potentially locally selected SNPs were identified. Candidate genes for local selection constituted a wide array of functions, including calcium signalling, neuroactive ligand–receptor interaction and circadian rhythm. Remarkably, one of the candidate genes identified is PERIOD, possibly related to differences in local photoperiod associated with the >30° difference in latitude between locations. Genes under selection were spread across the genome, and there were no large regions of increased differentiation as expected when selection occurs within just a single generation due to panmixia. This supports the conclusion that most of the genome is homogenized by gene flow that removes any effects of diversifying selection from each new generation.